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Neutrophil Elastase, Proteinase 3, and Cathepsin G as Therapeutic Targets in Human Diseases

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Abstract	727
I. Introduction	727
II. Neutrophil elastase, proteinase 3, and cathepsin G	728
A. History	728
B. Biosynthesis, processing, and localization in neutrophil	729
C. Structural characteristics and proteolytic specificity	731
D. Plasma membrane association	734
III. Biological functions of elastase, proteinase 3, and cathepsin G	735
A. Antimicrobial roles in infections	735
B. Roles in inflammatory process regulation	736
1. Processing of cytokines, chemokines, and growth factors	736
2. Processing and activation of cellular receptors	737
3. Induction of apoptosis by proteinase 3	738
IV. Physiological inhibitors of elastase, proteinase 3, and cathepsin G	738
A. Serine protease inhibitors	738
1. α 1-Protease inhibitor	739
2. α 1-Antichymotrypsin	740
3. Monocyte neutrophil elastase inhibitor, proteinase inhibitor 6, and proteinase inhibitor 9	740
B. Canonical inhibitors	740
1. Secretory leukocyte protease inhibitor	740
2. Elafin	741
C. α -Macroglobulins	741
V. Pathophysiology of elastase, proteinase 3 and cathepsin G in human diseases	742
A. Chronic inflammatory lung diseases	742
1. Chronic obstructive pulmonary disease	742
2. Cystic fibrosis	743
3. Acute lung injury and acute respiratory distress syndrome	744
B. Anti-neutrophil cytoplasmic autoantibody-associated vasculitides	744
C. Hereditary neutropenias	745
D. Papillon-Lefèvre syndrome	746
VI. New strategies for fighting neutrophil serine protease-related human diseases	746
A. Therapeutic inhibitors	746
B. Reducing intracellular levels of active elastase, proteinase 3, and cathepsin G	749
C. Reducing neutrophil accumulation at inflammatory sites	750

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VII. Concluding remarks.....	751
Acknowledgments.....	752
References	752

Abstract—Polymorphonuclear neutrophils are the first cells recruited to inflammatory sites and form the earliest line of defense against invading microorganisms. Neutrophil elastase, proteinase 3, and cathepsin G are three hematopoietic serine proteases stored in large quantities in neutrophil cytoplasmic azurophilic granules. They act in combination with reactive oxygen species to help degrade engulfed microorganisms inside phagolysosomes. These proteases are also externalized in an active form during neutrophil activation at inflammatory sites, thus contributing to the regulation of inflammatory and immune responses. As multifunctional proteases, they also play a regulatory role in noninfectious inflammatory diseases. Mutations in the *ELA2/ELANE* gene, encoding neutrophil elastase, are the cause of human congenital neutropenia. Neutrophil membrane-bound proteinase 3 serves

as an autoantigen in Wegener granulomatosis, a systemic autoimmune vasculitis. All three proteases are affected by mutations of the gene (*CTSC*) encoding dipeptidyl peptidase I, a protease required for activation of their proform before storage in cytoplasmic granules. Mutations of *CTSC* cause Papillon-Lefèvre syndrome. Because of their roles in host defense and disease, elastase, proteinase 3, and cathepsin G are of interest as potential therapeutic targets. In this review, we describe the physicochemical functions of these proteases, toward a goal of better delineating their role in human diseases and identifying new therapeutic strategies based on the modulation of their bioavailability and activity. We also describe how non-human primate experimental models could assist with testing the efficacy of proposed therapeutic strategies.

I. Introduction

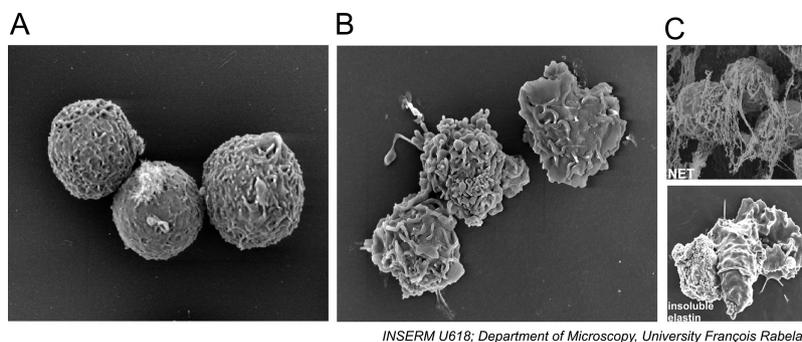
Human polymorphonuclear neutrophils represent 35 to 75% of the population of circulating leukocytes and are the most abundant type of white blood cell in mammals (Borregaard et al., 2005). They are classified as granulocytes because of their intracytoplasmic granule content and are characterized by a multilobular nucleus. Neutrophils develop from pluripotent stem cells in the bone marrow and are released into the bloodstream where they reach a concentration of 1.5 to 5×10^9 cells/liter. Their half-life in the circulation is only on the order of a few hours. They play an essential role in innate immune defense against invading pathogens and are among the primary mediators of inflammatory response. During the acute phase of inflammation, neutrophils are the first inflammatory cells to

leave the vasculature, where they migrate toward sites of inflammation, following a gradient of inflammatory stimuli. They are responsible for short-term phagocytosis during the initial stages of infection (Borregaard and Cowland, 1997; Hampton et al., 1998; Segal, 2005). Neutrophils use complementary oxidative and nonoxidative pathways to defend the host against invading pathogens (Kobayashi et al., 2005).

The three serine proteases neutrophil elastase (NE¹), proteinase 3 (PR3), and cathepsin G (CG) are major components of neutrophil azurophilic granules and participate in the nonoxidative pathway of intracellular and extracellular pathogen destruction. These neutrophil serine proteases (NSPs) act intracellularly within phagolysosomes to digest phagocytized microorganisms in combination with microbicidal peptides and the membrane-associated NADPH oxidase system, which produces reactive oxygen metabolites (Segal, 2005). An additional extracellular antimicrobial mechanism, neutrophil extracellular traps (NET), has been described that is made of a web-like structure of DNA secreted by activated neutrophils (Papayannopoulos and Zychlinsky, 2009) (Fig. 1). NETs are composed of chromatin bound to positively charged molecules, such as histones and NSPs, and serve as physical barriers that kill pathogens extracellularly, thus preventing further spreading. NET-associated NSPs participate in pathogen killing by degrading bacterial virulence factors extracellularly (Brinkmann et al., 2004; Papayannopoulos and Zychlinsky, 2009).

In addition to their involvement in pathogen destruction and the regulation of proinflammatory processes, NSPs are also involved in a variety of inflammatory human conditions, including chronic lung diseases (chronic obstructive pulmonary disease, cystic fibrosis,

¹ Abbreviations: α 1-PI, α 1-protease inhibitor; ACT, α 1-antichymotrypsin; ALI, acute lung injury; ANCA, anti-neutrophil cytoplasmic autoantibodies; AP, adaptor protein; ARDS, acute respiratory distress syndrome; BAL, bronchoalveolar lavage; cANCA, cytoplasmic ANCA; CHS, Chediak-Higashi syndrome; CF, cystic fibrosis; CFTR, cystic fibrosis transmembrane conductance regulator; CG, cathepsin G; COPD, chronic obstructive pulmonary disease; DPPI, dipeptidyl peptidase I; E-64, (2S,3S)-3-[[[(1S)-1-[[[4-[(aminoimino-methyl)amino]butyl]amino]carbonyl]-3-methylbutyl]amino]carbonyl]-2-oxiranecarboxylic acid; FRET, fluorescence resonance energy transfer; HNE, human neutrophil elastase; IL, interleukin; LPS, lipopolysaccharide; MMP, matrix metalloprotease; mPR3, membrane-bound proteinase 3; NE, neutrophil elastase; NET, neutrophil extracellular trap; NF κ B, nuclear factor κ B; NSP, neutrophil serine protease; pANCA, perinuclear ANCA; PAR, protease-activated receptor; PDE4, phosphodiesterase E4; PI, protease inhibitor; PLS, Papillon-Lefèvre syndrome; PR3, proteinase 3; RBL, rat basophilic leukemia; RCL, reactive center loop; SDF, stromal cell-derived factor; Serpin, serine protease inhibitor; SLPI, secretory leukocyte protease inhibitor; TIMP, tissue inhibitor of metalloproteases; TLR, Toll-like receptor; TNF, tumor necrosis factor; WG, Wegener granulomatosis.



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FIG. 1. Polymorphonuclear neutrophil. Quiescent (A) and chemically activated (B) neutrophils purified from peripheral blood. C, PMA-activated neutrophils embedded within NET and neutrophil spreading on insoluble elastin.

acute lung injury, and acute respiratory distress syndrome) (Lee and Downey, 2001; Shapiro, 2002; Moraes et al., 2003; Owen, 2008b). In these disorders, accumulation and activation of neutrophils in the airways result in excessive secretion of active NSPs, thus causing lung matrix destruction and inflammation. NSPs are also involved in other human disorders as a consequence of gene mutations, altered cellular trafficking, or, for PR3, autoimmune disease. Mutations in the *ELA2/ELANE* gene encoding HNE are the cause of human cyclic neutropenia and severe congenital neutropenia (Horwitz et al., 1999, 2007). Neutrophil membrane-bound proteinase 3 (mPR3) is the major target antigen of anti-neutrophil cytoplasmic autoantibodies (ANCA), which are associated with Wegener granulomatosis (Jenne et al., 1990). All three proteases are affected by mutation of the gene (*CTSC*) encoding dipeptidyl peptidase I (DPPI), which activates several granular hematopoietic serine proteases (Pham and Ley, 1999; Adkison et al., 2002). Mutations of *CTSC* cause Papillon-Lefèvre syndrome and palmoplantar keratosis (Hart et al., 1999; Toomes et al., 1999).

In this review, we focus on the physicochemical properties of HNE, PR3, and CG, drawing attention to recent advances in their physiopathological functions to better understand their role in human diseases. We propose and discuss new therapeutic strategies based on modulation of their activity. We also describe how nonhuman primate models of NSPs-related human diseases could help test the efficacy of therapeutic approaches.

II. Neutrophil Elastase, Proteinase 3, and Cathepsin G

A. History

Proteases are proteolytic enzymes that catalyze the splitting of proteins into smaller peptides or amino acids and are important in many ways to human health and biotechnology. Four major classes of proteases are distinguished on the basis of key residues involved in catalysis: serine proteases, cysteine proteases, aspartic acid proteases, and metalloproteases. A new type of catalysis that involves a threonine in the catalytic site has been

identified more recently in studies of the proteasome. There are at least 500 to 600 different proteases in humans; most of them are serine, cysteine, and metalloproteases (López-Otín and Bond, 2008). The serine endopeptidases (EC 3.4.21.-) are characterized by the presence of a conserved serine residue as part of the catalytic center. In trypsin/chymotrypsin-type serine proteases, for example, this catalytic triad consists of the three residues Asp, His, and Ser (Polgár, 2005). The major clans found in humans include chymotrypsin-like, α/β -hydrolase, and signal peptidase. Serine proteases represent approximately one third of total proteases currently identified and are present in eukaryotes, prokaryotes, bacteria, and archaea (Hedstrom, 2002). They display diverse biological functions and include digestive enzymes of exocrine glands, clotting factors, and leukocyte granule-associated proteases, such as NE, PR3, and CG.

Although the activity of leukocyte proteases had been described early in the 20th century, HNE was identified only in 1968 by Janoff and Scherer (1968). The term “elastase” is used to describe an enzyme capable of releasing soluble peptides from insoluble elastin, which was the first substrate employed for characterizing its activities, but does not necessarily imply that its activities are always physiologically related to digestion of this target. Subsequently, another protease retaining enzymatic activity on synthetic substrates for chymotrypsin was described (Dewald et al., 1975; Rindler-Ludwig and Braunsteiner, 1975) and designated “cathepsin G” (Starkey and Barrett, 1976). A third protease, “myeloblastin,” was first identified in 1978 and more extensively characterized 10 years later. This name was originally used by Bories et al. (1989) to describe a serine protease in promyelocytic leukemia cells HL-60. It was subsequently shown that myeloblastin was identical to a protease known independently as “proteinase 3” that had been studied for its role in emphysema (Baggiolini et al., 1978). The same molecule had been also described as a protein with antimicrobial activity (Campanelli et al., 1990a) and called azurophilic granule protein 7, and it was identified as the p29 autoantigen or ANCA auto-antigen in Wegener granulo-

matosis before it finally became referred to uniformly as “proteinase 3.”

B. Biosynthesis, Processing, and Localization in Neutrophil

HNE, PR3, and CG are three homologous proteases that belong to the chymotrypsin superfamily of serine proteases. They evolved from a common ancestor through gene duplication. The genes encoding HNE, PR3, and CG consist of five exons and four introns (Zimmer et al., 1992; Caughey et al., 1993). The gene for HNE, formerly called *ELA2* and newly officially dubbed *ELANE*, is located in the same cluster as that of PR3 (*PRTN3*) and azurocidin in the terminal region of the short arm of chromosome 19p13.3 (Zimmer et al., 1992; Caughey et al., 1993). In contrast to its related family members, azurocidin has lost its catalytic serine and is devoid of proteolytic activity (Watorek, 2003). It primarily exhibits antimicrobial function. The CG gene (*CTSG*) is located on chromosome 14q11.2 in a cluster containing other genes for the related serine proteases

chymase, granzyme H (Fellows et al., 2007), and granzyme B (Caughey et al., 1993). HNE, PR3, and CG genes are expressed in granulocytes, monocytes, and mast cells. High-level transcription of these HNE, PR3, and CG genes is limited to the promyelocytic stage of neutrophil maturation (Garwicz et al., 2005). PR3 is also found in basophiles (Braun et al., 1991). The main characteristics of HNE, PR3, and CG are presented in Table 1.

The synthesis of HNE, PR3, and CG is regulated first at the transcriptional level during granulocyte development and second at the post-translational level before they are stored in their proteolytically active mature form within neutrophil azurophilic granules. They are synthesized as an inactive prepro-protein containing a signal peptide and an amino-terminal prodipeptide (Rao et al., 1996; Garwicz et al., 1997, 1998; Gullberg et al., 1997). They also contain a C-terminal propeptide, the removal of which is not necessary for NSP activity. The processing and granule targeting of NSPs has been studied in transfected cells producing active proteases in a

TABLE 1
Main characteristics of elastase, proteinase 3, and cathepsin G

Characteristic	Elastase	Proteinase 3	Cathepsin G
EC number	3.4.21.37	3.4.21.76	3.4.21.20
Gene locus and gene structure	19p13.3, 5 exons 4 introns	19p13.3, 5 exons 4 introns	14q11.2, 5 exons 4 introns
Endogenous activator	Dipeptidyl peptidase I	Dipeptidyl peptidase I	Dipeptidyl peptidase I
Prodipeptide	Ser-Glu	Ala-Glu	Gly-Glu
Characteristics of mature forms			
Residues	218	222	235
Molecular mass	29–33 kDa	29–32 kDa	28.5 kDa
pI	~10.5	~9.5	~12
Number of glycosylation sites	2	2	1
Number of disulfide bridges	4	4	3
Optimal pH for activity	8.0–8.5	~8.0	~7.5
Substrate specificity	Small hydrophobic residue at P1 position: Val, Cys, Ala, Met, Ile, Leu, Ser	Small hydrophobic residue at P1 position: Val, Cys, Ala, Met, Ser, Leu	Aromatic or positively charged residues at P1 position: Phe, Tyr, Lys, Arg
Best FRET substrate	Abz-APEELMRRQ-EDDnp	Abz-VADnorVADYQ-EDDnp	Abz-EPFWEDQ-EDDnp
Localization in neutrophil	Azurophilic granules Nuclear envelope Neutrophil cell surface after priming Neutrophil extracellular traps	Azurophilic granules Specific granules Secretory vesicles On quiescent and activated neutrophil cell surface Neutrophil extracellular traps	Azurophilic granules Neutrophil cell surface after priming Neutrophil extracellular traps
Source	Neutrophil Monocyte	Neutrophil Monocyte Basophil	Neutrophil Monocyte Mastocyte
Endogenous inhibitors	α 2-Macroglobulin α 1-PI/MNEI/PI9 SLPI/Elafin/pre-elafin	α 2-Macroglobulin α 1-PI/MNEI Elafin/pre-elafin	α 2-Macroglobulin ACT/MNEI/ α 1-PI/PI6 SLPI
Biologicals functions	Degradation of ECM components Bactericidal properties Cleavage of inflammatory mediators Cleavage of receptors Cleavage of lung surfactant Cytokine and chemokine induction Induction of airway submucosal gland secretion	Degradation of ECM components Bactericidal properties Cleavage of inflammatory mediators Cleavage of receptors Induction of endothelial cell apoptosis Negative feedback regulation of granulopoiesis	Degradation of ECM components Bactericidal properties Cleavage of inflammatory mediators Cleavage of receptors Platelet activation Induction of airway submucosal gland secretion
Pathological roles in human diseases	Inflammatory diseases Papillon-Lefèvre syndrome Hereditary neutropenia	Inflammatory diseases Papillon-Lefèvre syndrome Wegener's granulomatosis	Inflammatory diseases Papillon-Lefèvre syndrome

fashion similar to that of human neutrophils. Activation of NSPs occurs through cleavage of the amino-terminal peptide by signal peptidase, followed by the removal of an aminoterminal dipeptide by DPPI, a tetrameric cysteine protease also known as cathepsin C (EC 3.4.14.1). DPPI is a highly conserved lysosomal cysteine exopeptidase expressed mostly in the lung, spleen, kidney, and myeloid cells and belongs to the papain family (McGuire et al., 1993). It is composed of an oligomeric structure derived from four identical subunits and represents the only member of this family that is functional as a tetramer (Turk et al., 2001). DPPI is initially synthesized as a 55-kDa monomeric pro-enzyme rapidly processed to generate a mature form, but the regulation of its processing is still unknown. The proteolytically active enzyme adopts a papain like-structure made of a 23-kDa

heavy chain (Leu207–Arg370) and a 7-kDa light chain (Asp371–Leu439) linked by disulfide bonds and an “exclusion” propeptide domain of 16 kDa (Asp1–Gly119) that remains bound to the mature active enzyme (Fig. 2A). This so-called exclusion domain transforms the framework of a papain-like endopeptidase into a dipeptidyl exopeptidase by blocking the active site beyond the S2 pocket (Turk et al., 2001) (Fig. 2B). In addition to its key role as an activator of hematopoietic granule serine proteases, DPPI also participates in lysosomal peptide degradation via its dipeptidyl peptidase activity. The enzyme cleaves two-residue units from the N termini of proteins until it reaches a stop sequence, typically an arginine or lysine in P2, a proline residue in P1 or P1', or an isoleucine residue in P1. The C-terminal propeptide of HNE, PR3, and CG is normally excised by an as-yet-

A

pro-dipeptidyl peptidase I

DTPNACTYLDLLGTWVVFQVGSQSDVNCVSMGPPQEKVVVYLQKLDAYDDLGNLSGHFTIIY
 NQGFEIVLNDYKWFVAFKFKYKEEGSKVTTYCNETMTGWVHDVLRNHWACFTGKKVGTASENVVYN
 TAHLKNSQEKYSNRLYKYDHNFKVKA INAIQKSWTATTYMEYETLLTGLDMIRRSRGGHSRKRIPRK
 PAPLTAEIQQKILHLPTSWDWRNVHGINFVSPVRNQASCSCYFASMGMLEARIRILTNNSQT
 PILSPQEVVSCSQYACQCEGGFPYLIAGKYAQDFGLVEEACFPYTGTDSPCKMKEDCFRYSSE
 YHYVGGFYGGCNEALMKLELVHVGPMVAFAFEVYDDFLHYKKG IYHHTGLRDPFNPFLTNHAVL
 LVGYGTDASAGMDYIVKNSWGTGWGENGYFRIRRGTDCAIESIAVAATPIPKL

Exclusion domain (Asp1–Gly119)
 Activation peptide (Thr120–His206)
 Heavy chain (Leu207–Arg370)
 Light chain (Asp371–Leu439)

B

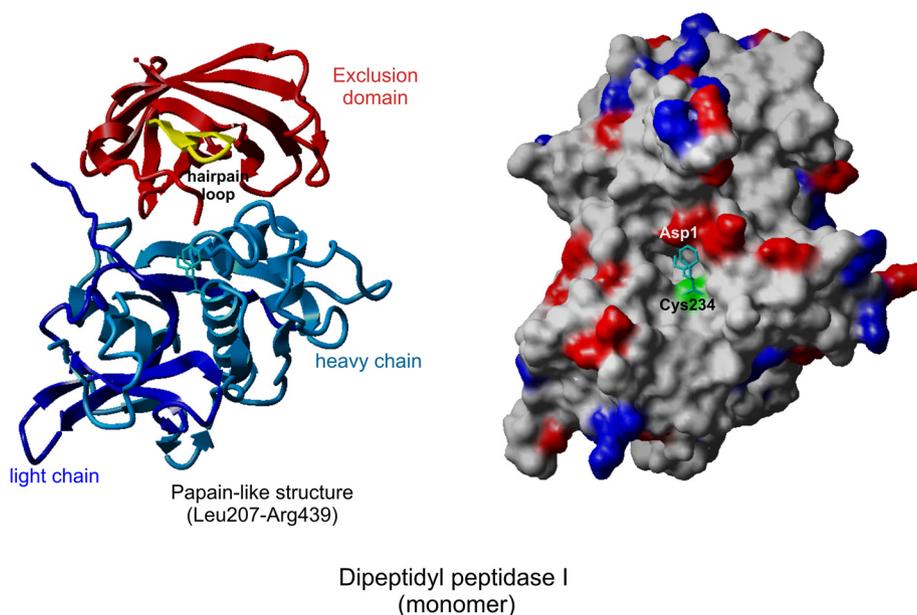


FIG. 2. Structure of human pro-dipeptidyl peptidase I. A, amino acid sequence of human pro-dipeptidyl peptidase I. Primary sequences corresponding to exclusion domain (Asp1–Gly119), activation peptide (Thr120–His206), heavy chain (Leu207–Arg370), and light chain (Asp371–Leu439) are colored in red, gray, light, and dark blue, respectively. B, ribbon representation and solvent-accessible surfaces of the DPPI functional monomer in complex with the inhibitor Gly-Phe-CHN₂ [Protein Data Bank 1K3B (Turk et al., 2001), 2DJF, and 2DJG (Mølgaard et al., 2007)]. Color codes in the ribbon plot are the same as in A except that Asp1 in the hairpin loop is colored yellow (left). Solvent-accessible surfaces with positive or negative electrostatic potential are colored dark blue and red, respectively (right). The side chain of the catalytic Cys234 is shown with a cyan stick. The figures have been created with Yasara (<http://www.yasara.org>).

unknown protease(s), although this does not seem to be required for either granule targeting or proteolytic activity (Gullberg et al., 1995; Capizzi et al., 2003).

Fully processed mature HNE, PR3, and CG isolated from azurophilic granules contain, respectively, 218 (Bode et al., 1986; Sinha et al., 1987), 222 (Campanelli et al., 1990b), and 235 (Salvesen et al., 1987; Hof et al., 1996) residues. They are present in several isoforms depending on their carbohydrate content, with apparent mass of 29 to 33 kDa upon SDS-polyacrylamide gel electrophoresis (Twumasi and Liener, 1977; Watorek et al., 1993). HNE and PR3 display two sites of N-glycosylation, whereas CG possesses only one. NSPs are stored mainly in neutrophil azurophilic granules, but HNE is also localized in the nuclear envelope, as revealed by immunostaining and electron microscopy (Clark et al., 1980; Benson et al., 2003), whereas PR3 is also found in secretory vesicles (Witko-Sarsat et al., 1999a). Upon neutrophil activation, granular HNE, PR3, and CG are secreted extracellularly, although some molecules nevertheless remain at the cell surface (Owen and Campbell, 1999; Owen, 2008a). The mechanism through which NSPs are sorted from the *trans*-Golgi network to the granules has not been completely defined, even though an intracellular proteoglycan, serglycin, has been identified as playing a role in elastase sorting and packaging into azurophilic granules (Niemann et al., 2007). Unlike HNE and CG, PR3 is constitutively expressed on the membranes of freshly isolated neutrophils (Csernok et al., 1990; Halbwachs-Mecarelli et al., 1995). Stimulation of neutrophils at inflammatory sites triggers intracytoplasmic granules to translocate to the phagosomes and plasma membrane, thereby liberating their contents. The first step of the translocation to the target membrane depends on cytoskeleton remodeling and microtubule assembly (Burgoyne and Morgan, 2003). This is followed by a second step of granule tethering and docking, which are dependent on the sequential intervention of SNARE proteins (Jog et al., 2007).

C. Structural Characteristics and Proteolytic Specificity

As found for other members of this family (i.e., the chymotrypsin/trypsin-type family), HNE, PR3, and CG display a three dimensional structure consisting of two homologous β -barrels and a C-terminal α -helix (Bode et al., 1986; Fujinaga et al., 1996; Hof et al., 1996) (Fig. 3A). Each barrel contains six antiparallel β -sheets connected through a linker segment. Residues of the catalytic triad [Ser195, Asp102, and His57 (chymotrypsin numbering)] are located at the junction of the two β -barrels, whereas the active site cleft runs perpendicular to this junction. This arrangement of amino acids in the active site presumably allows nucleophilic attack by Ser195 on the carbonyl carbon (C = O) of the substrate scissile bond, thus setting off the catalysis process.

Upon processing of a dipeptide at the amino terminus of NSPs by DPPI, the free ammonium group of the first N-terminal residue (Ile16) forms an internal salt bridge with the side-chain carboxylate of Asp194 that renders the active site S1 pocket [Schechter and Berger (1967) nomenclature; Fig. 4A] accessible to substrate. Ile16 together with the three flexible surface loops (217–225 loop, 180 loop, and autolysis loop) of the C-terminal β -barrel form the activation domain of NSPs (Fig. 3A), the conformation of which differs after processing by DPPI. The main differences between the topologies of pro- and mature forms of related serine proteases have been previously documented for thrombin, prochymase, and progranzyme K (Hink-Schauer et al., 2002; Reiling et al., 2003; Jenne and Kuhl, 2006). HNE, PR3, and CG are highly cationic proteases as a result of their content of positively charged residues. HNE and PR3 display a cluster of positively charged residues located in the loops of the activation domain (Korkmaz et al., 2007). This positive cluster is disrupted by negatively charged residues in PR3. Four of the five hydrophobic residues forming the surface hydrophobic patch in PR3 are located on loop 217–225 (Fig. 3B). This most probably explains the specific binding of mature PR3 but not of its proform to the neutrophil membrane (Korkmaz et al., 2008b).

The three dimensional structure of the chymotrypsin family of serine proteases in complex with inhibitors provides useful information regarding the operation of the active site. Structures of HNE in complex with turkey ovomucoid third domain (Bode et al., 1986), secretory leukocyte protease inhibitor (SLPI) domain 2 (Kozumi et al., 2008), and synthetic chloromethyl ketone inhibitors (Wei et al., 1988; Navia et al., 1989) have been determined as that of CG in complex with Suc-Val-Pro-PheP-(O⁺Ph)₂ (Hof et al., 1996) and β -ketophosphonate 1 (de Garavilla et al., 2005). The crystal structure of PR3 has been solved by molecular replacement using the crystallized HNE structure (Fujinaga et al., 1996). HNE, PR3, and CG display a common fold, but their distinct properties with respect to particular substrate cleavage specificity arises from the substitutions in the S1 pocket and also from the surface loops surrounding the active site (99 loop, 60 loop, 37 loop, and autolysis loop) defining the environment of the active site. Solvent-accessible surfaces in HNE, PR3, and CG show that their charge distributions differ significantly in the vicinity of the substrate binding region (Korkmaz et al., 2008c).

The S1 pocket in individual chymotrypsin-like serine proteases plays an important role in defining their substrate specificity. The HNE S1 pocket is hemispherical and hydrophobic because of the presence of Val190, Phe192, Ala213, Val216, Phe228, and the disulfide bridge Cys191–Cys220 (Bode et al., 1986). The S1 pocket of PR3 is also hemispherical but seems to be smaller than that of HNE because of the Val/Ile substitution at position 190 (Fujinaga et al., 1996). The S1 subsite of CG, which is larger than that of

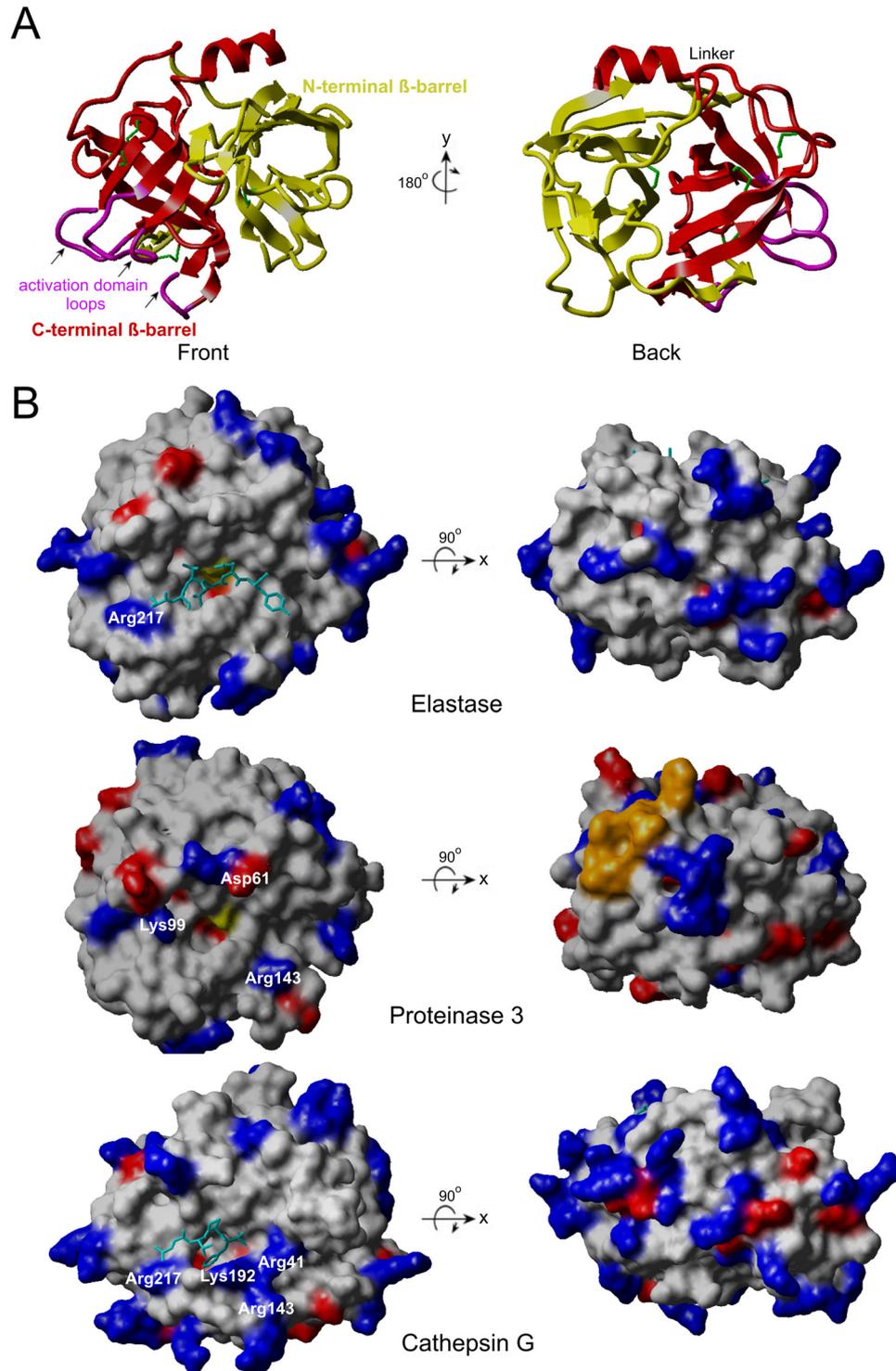


FIG. 3. Three-dimensional architecture of the trypsin/chymotrypsin family and structural differences between neutrophil elastase, proteinase 3, and cathepsin G. A, ribbon plot of neutrophil elastase showing the characteristics of the trypsin/chymotrypsin family, the two asymmetric β -barrels and the C-terminal α -helix, front view on the left, back view after a rotation of 180° around a vertical y -axis on the right. N- and C-terminal β -barrels are presented in red and yellow, respectively. The three flexible loops of the C-terminal β -barrels forming the activation domain are colored in pink and indicated by arrows. Disulfide bonds are depicted in green. B, the solvent accessible surface based on the atom coordinates of elastase [Protein Data Bank 1PPF (Bode et al., 1986)], proteinase 3 [Protein Data Bank 1FUJ (Fujinaga et al., 1996)], and cathepsin G [1CGH (Hof et al., 1996)] is colored to show its positive (blue) and negative (red) electrostatic potential. Surface-accessible residues forming a hydrophobic patch on proteinase 3 are depicted in orange. The loop of the inhibitor turkey ovomucoid third domain (P4–P3') complexed to elastase and the irreversible phosphonate inhibitor Suc-Val-Pro-Phe^P-(OPh)₂ complexed to cathepsin G are given as a cyan stick model. The serine of the catalytic triad is yellow. Ribbon plot of neutrophil elastase and the molecular surfaces are generated with Yasara (<http://www.yasara.org>).

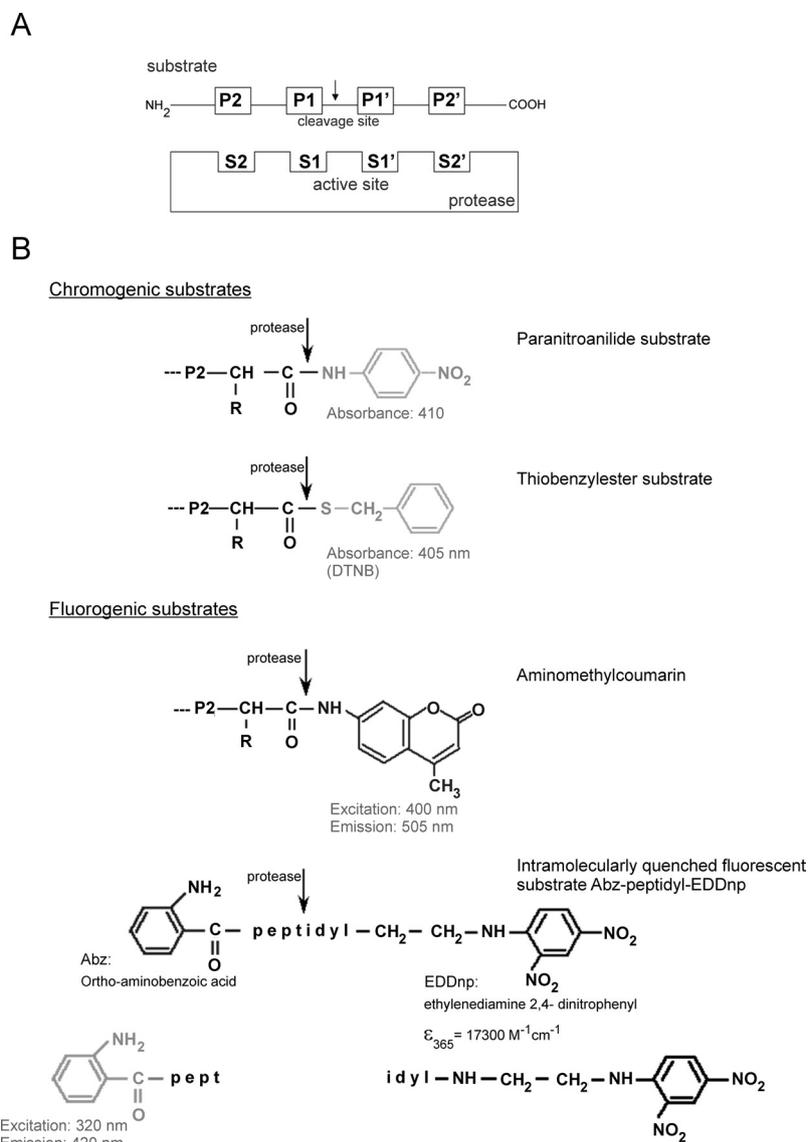


FIG. 4. Synthetic chromogenic and fluorogenic substrates of NSP. A, schematic diagram illustrating the Schechter and Berger (1967) nomenclature. This nomenclature defines a linear topology of the interactions between a protease and a substrate: S subsites on the protease accommodate P residues of the substrate upstream of the scissile bond, whereas S' subsites accommodate P' residues from the C-terminal part of the substrate, downstream of the cleavage site. Numbering starts with the first residue next to the cleavage site, P1 and P1', and continues toward the N terminus (P2, P3, P4, etc.) and the C terminus (P2', P3', P4', etc.). B, chromogenic substrates commonly used to measure the activity of NSPs, peptidyl-paranitroanilides (top), peptidyl-thiobenzylesters with chromogenic groups in gray. Paranitroanilide may be detected by direct measurement at 410 nm, but a coupled assay with a thiodisulfide reagent such as DTNP is required for measuring the absorbance of the released thiobenzyl group. Fluorogenic aminomethylcoumarin substrates contain a fluorescent group that is released by proteolytic cleavage. FRET substrates contain a fluorescent and a quenching group as a donor/acceptor pair [here a fluorescent *ortho*-aminobenzoyl (Abz) group and a *N*-(2,4-dinitrophenyl ethylenediamine (EDDnp) quenching group] at their N- and C-terminal ends, respectively. Fluorescence is released after cleavage of any peptide bond within the amino acid sequence (shown in gray). FRET substrates are convenient tools to investigate the protease specificity around the cleavage site. DTNB, 5,5'-dithiobis(2-nitrobenzoic acid).

HNE and PR3, is divided into two compartments with a negatively charged Glu226 at the bottom (Hof et al., 1996). The specificity of NSPs has been investigated using chromogenic (p-nitroanilide, Anb^{5,2}-NH₂, thiobenzylester) and fluorogenic [aminomethylcoumarin, fluorescence resonance energy transfer (FRET)] substrates (Castillo et al., 1979; Nakajima et al., 1979; McRae et al., 1980; Tanaka et al., 1985; Brubaker et al., 1992; Kam et al., 1992; Réhault et al., 1999; Wysocka et al., 2007; Korkmaz et al., 2008a; Carmona et al., 2009) (Fig. 4B). In agreement with structural data, HNE and PR3 preferen-

tially accommodate small hydrophobic residues (Val, Cys, Ala, Met, Ile) (Brubaker et al., 1992; Koehl et al., 2003; Korkmaz et al., 2007; Wysocka et al., 2007) in the S1 pocket, whereas CG has both a chymotrypsin-like and a trypsin-like specificity, permitting both large, hydrophobic P1 residues (Phe, Leu, Met) and positive Lys or Arg residues (Tanaka et al., 1985). The S2 subsites of HNE and CG are bordered by Phe215, Leu99, and the flat side of the imidazole ring of the catalytic triad His57, which is quite hydrophobic. In contrast, the S2 subsite of PR3 is a deep polar pocket of increased polarity as a result of the Leu-to-

Lys substitution at position 99 (Fujinaga et al., 1996). The size and hydrophobic properties of the S2 subsite of HNE and CG account for the fact that medium-sized hydrophobic side chains, such as that of Pro, are preferred at the P2 position (Tanaka et al., 1985; Réhault et al., 1999). Indeed, most commercially available chromogenic and/or fluorogenic substrates used to measure HNE and CG display a proline at the P2 position. Because of the presence of Lys99, PR3 preferentially accommodates a negatively charged residue at P2 (Hajjar et al., 2006; Korkmaz et al., 2007). The S3 subsite of CG is formed by a Lys at position 192, which favors interaction with an acidic P3 residue (Tanaka et al., 1985). The residue at position 99 in all three proteases borders both the S2 and S4 subsites, which makes it smaller and more polar in PR3 than in HNE or CG because of the Leu-to-Lys substitution. Regarding the S' subsites, the S1' and S2' subsites in HNE are relatively hydrophobic and lined with Cys42–Cys58 and Phe41, Leu143, respectively. The S2' subsite in PR3 lies in the vicinity of the charged residues Asp61 and Arg143, neither of which is conserved in HNE (Fujinaga et al., 1996). The 60 loop in PR3 containing Asp61 is significantly displaced to bring the negatively charged side chain to the S1' and S3' sites, thereby making them smaller and more polar. These peculiarities have been exploited to develop the first specific synthetic substrates of human PR3 (Korkmaz et al., 2004, 2007). It is noteworthy that Asp61 and Arg143 are conserved in mouse and human PR3, whereas the Lys99–Arg60 doublet in human is replaced by Asn99–Gln60 in the mouse (Fig. 5A), which explains why mouse PR3 does not cleave human PR3 substrates bearing a negatively charged residue at P2 (Kalupov et al., 2009) (Fig. 5B). The P'–S' specificity of CG has not yet been fully elucidated. X-ray structural analysis showed that CG displays two positively charged residues (Arg41 and Arg143) that reside in the immediate vicinity of the active S2' site and that could contribute to the specificity of the protease (Hof et al., 1996; Réhault et al., 1999).

D. Plasma Membrane Association

Exposure of neutrophils to cytokines (TNF- α), chemoattractants (platelet-activating factor, formyl-Met-Leu-Phe, or IL-8), or bacterial lipopolysaccharide leads to rapid granule translocation to the cell surface with secretion of HNE, PR3, and CG into the extracellular medium (Owen and Campbell, 1999). A fraction of secreted HNE, PR3, and CG is detected at the surface of activated neutrophils (Owen et al., 1995a, 1997; Campbell et al., 2000). Resting purified neutrophils from peripheral blood express variable amounts of PR3 on their surface. A bimodal, apparently genetically determined, distribution has been observed with two populations of quiescent neutrophils that express or do not express the protease at their surface (Halbwachs-Mecarelli et al., 1995; Schreiber et al., 2003). The percentage of mPR3-positive neutrophils ranges from 0 to 100% of the total neutrophil population within individuals. Furthermore,

the percentage of mPR3-positive neutrophils remains stable over time and is not affected by neutrophil activation (Halbwachs-Mecarelli et al., 1995).

The mechanism through which HNE and CG are associated with the outer surface of the plasma membrane of neutrophils mainly involves electrostatic interactions with the sulfate groups of chondroitin sulfate- and heparan sulfate-containing proteoglycans (Campbell and Owen, 2007). These two proteases are released from neutrophil cell surfaces by high concentrations of salt (Owen et al., 1995b, 1997; Korkmaz et al., 2005a) and after treatment with chondroitinase ABC and heparinase (Campbell and Owen, 2007). Membrane PR3 is not solubilized by high salt concentrations, which means that its membrane association is not charge dependant (Witko-Sarsat et al., 1999a; Korkmaz et al., 2009). Unlike HNE and CG, PR3 bears at its surface a hydrophobic patch formed by residues Phe166, Ile217, Trp218, Leu223, and Phe224 that is involved in membrane binding (Goldmann et al., 1999; Hajjar et al., 2008) (Fig. 3B). Several membrane partners of PR3 have been identified, including CD16/Fc γ RIIIb (David et al., 2005; Fridlich et al., 2006), phospholipid scramblase-1, a myristoylated membrane protein with translocase activity present in lipid rafts (Kantari et al., 2007), CD11b/CD18 (David et al., 2003), and human neutrophil antigen NB1/CD177 (von Vietinghoff et al., 2007; Hu et al., 2009), a 58- to 64-kDa glycosyl-phosphatidylinositol anchored surface receptor belonging to the urokinase plasminogen activator receptor superfamily (Stroncek, 2007). NB1 shows a bimodal distribution that superimposes with that of PR3 on purified blood neutrophils (Bauer et al., 2007). Active, mature forms of PR3 but not pro-PR3 can bind to the surface of NB1-transfected human embryonic kidney 293 cells (von Vietinghoff et al., 2008) and Chinese hamster ovary cells (Korkmaz et al., 2008b). Interaction involves the hydrophobic patch of PR3 because specific amino acid substitutions disrupting this patch in the closely related gibbon PR3 prevent binding to NB1-transfected cells (Korkmaz et al., 2008b). Decreased interaction of pro-PR3 with NB1-transfected cells is explained by the topological changes affecting the activation domain containing the hydrophobic patch residues. Together, these results support the hydrophobic nature of PR3-membrane interaction.

Because a significant fraction of HNE, PR3, and CG is detected at the surface of activated neutrophils, measuring and quantifying membrane-bound activities is of major interest for understanding their role during inflammation. The availability of sensitive and specific FRET substrates for each NSP has allowed the quantification of active proteases on the surface of stimulated neutrophils (Owen et al., 1995a, 1997; Korkmaz et al., 2005a, 2009). With the use of PR3-specific FRET substrate, it has been shown that constitutively expressed PR3 on the surface of quiescent blood neutrophils is

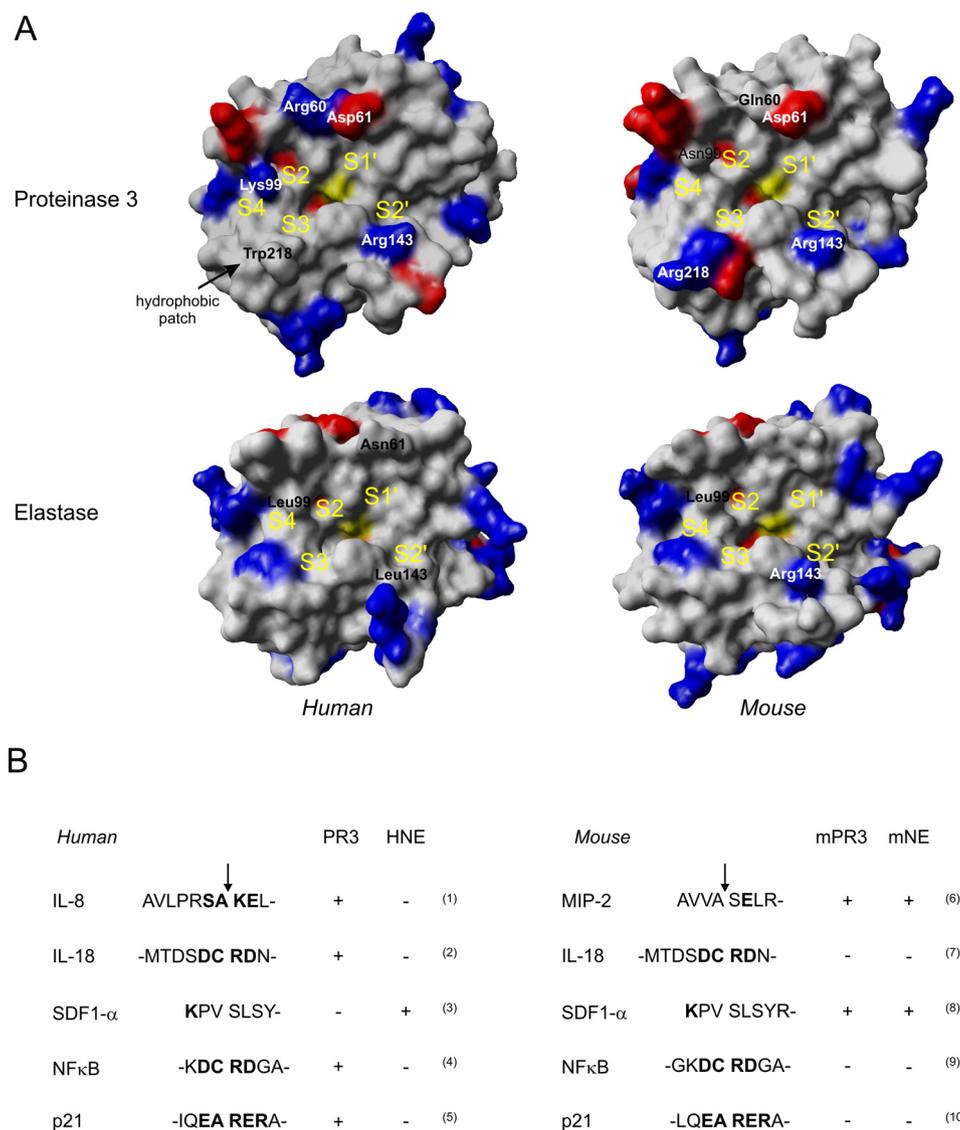


FIG. 5. A, interspecies comparisons of the active site region of proteinase 3 and neutrophil elastase from men and mice. Values of electrostatic potential were mapped onto the solvent accessible surface of each protease with positively and negatively charged residues colored in blue and red, respectively. Positions of the subsites S4 to S2' are shown in yellow. Key residues that lie in close vicinity to the substrate binding pockets are labeled by their three-letter codes. The hydrophobic patch in human PR3 is missing in the mouse homolog as the Trp218 residue is substituted by an Arg. B, sequences derived from natural human and mouse substrates that are cleaved by human and murine NE and PR3. Arrows indicate identified and potential cleavage sites. IL-8: (Padrines et al., 1994) (1); IL-18: putative cleavage sites [(2) and (7)]; SDF1- α : (Valenzuela-Fernandez et al., 2002) (3), putative cleavage site (8); NF κ B: (Preston et al., 2002) (4), NF κ B (Kalupov et al., 2009) (9); p21 (Dublet et al., 2005) (5), T. Kalupov et al., unpublished data (10); and MIP-2 (T. Dau and D. E. Jenne, unpublished data) (6). The structural models of murine proteases were derived from X-ray structures of human homologs by homology modeling (<http://www.expasy.ch>).

either enzymatically inactive or is unable to interact with substrates (Korkmaz et al., 2009).

III. Biological Functions of Elastase, Proteinase 3, and Cathepsin G

NSPs are currently viewed as multifunctional enzymes involved in pathogenic agent killing and in inflammatory process regulation (Pham, 2006). First recognized as degradative enzymes able to kill pathogens and cleave extracellular matrix components, NSPs have been attributed a potential role in chemotaxis and migration through cleavage of adhesion molecules at intercellular junctions (Cepinskas et al., 1999; Hermant et

al., 2003). This function, however, remains debated because some studies demonstrated decreased neutrophil chemotaxis when using NSP inhibitors (Stockley et al., 1990; Lomas et al., 1995; Young et al., 2007), whereas others have revealed no alteration of neutrophil migration in response to neutrophil-specific chemotactic stimuli in animal models deficient in NSPs (MacIvor et al., 1999; Adkison et al., 2002; Allport et al., 2002).

A. Antimicrobial Roles in Infections

HNE, PR3, and CG participate in direct intracellular killing of phagocytosed bacteria in phagolysosomes in combination with myeloperoxidase and reactive oxygen

species generated by the NADPH oxidase complex (Kobayashi et al., 2005). In addition to intracellular killing, extracellular killing can occur through trapping of bacteria in NET composed of filamentous DNA structures decorated with cationic proteases, including NSP secreted by activated neutrophils (Brinkmann et al., 2004). HNE exerts its antimicrobial activity on Gram-negative bacteria by cleaving the outer membrane protein A of *Escherichia coli* (Belaouaj et al., 2000) and other virulence factors of *Salmonella enterica*, *Yersinia enterocolitica*, and *Shigella flexneri* (Weinrauch et al., 2002). HNE also prevents the escape of *S. flexneri* from phagolysosomes in neutrophils (Weinrauch et al., 2002). Extracellular HNE and CG cleave the proinflammatory bacterial virulence factor flagellin (López-Boado et al., 2004) and degrade leukotoxin, a membrane pore-forming virulence factor of the Gram-negative bacteria *Actinobacillus actinomycetemcomitans*, which can lyse leukocytes and inhibit neutrophil functions (Tsai et al., 1979; Johansson et al., 2000). This pathogen has attracted attention because of its implication in severe destructive periodontal disease. However, the proteolytic activity of NSPs is not necessarily crucial for their antimicrobial activity. Their positive surface charges mediate strong binding to bacterial membranes. This binding alone may inhibit bacterial protein synthesis and induces membrane depolarization and disruption (Zasloff, 2002). Several peptides derived from the CG structure possess antimicrobial properties in vitro (Shafer et al., 1996, 2002). The antimicrobial properties of PR3 are also independent of its protease activity. PR3 efficiently kills both Gram-negative bacteria such as *E. coli* and Gram-positive bacteria such as *Streptococcus faecalis*, as well as fungi such as *Candida albicans*. PR3 also processes human cathelicidin (hCAP18) to its active LL-37 form in the extracellular environment after neutrophil activation (Sørensen et al., 2001). Human cathelicidin is an 18-kDa cationic anti-bacterial protein produced by epithelial cells of the gastrointestinal and respiratory tract and by sebocytes of the skin but also by blood cells, including neutrophils (Doss et al., 2010). Antimicrobial activity requires a proteolytic cleavage of hCAP-18 to liberate the active C-terminal 37-residue polypeptide that exerts broad antimicrobial activity against Gram-negative and -positive bacteria (Dürr et al., 2006).

Mice deficient in NE and CG have been employed as models for exploring their antibacterial functions in microbial infectious diseases. Previous studies showed that mice deficient in NE and CG are more susceptible to infection by Gram-negative and -positive bacteria (Reeves et al., 2002). In neutrophils from NE-deficient [NE(-/-)] mice infected by *S. flexneri*, 12% of bacteria escaped from the phagolysosome (Weinrauch et al., 2002).

B. Roles in Inflammatory Process Regulation

NSPs are abundantly secreted into the extracellular environment upon neutrophil activation at inflammatory sites. A fraction of the released proteases remain bound in an active form on the external surface of the plasma membrane so that both soluble and membrane-bound NSPs are able to proteolytically regulate the activities of a variety of chemokines, cytokines, growth factors, and cell surface receptors. Secreted proteases also activate lymphocytes and cleave apoptotic and adhesion molecules (Bank and Ansorge, 2001; Pham, 2006; Meyer-Hoffert, 2009). Thus, they retain pro- and anti-inflammatory activities, resulting in a modulation of the immune response at sites of inflammation.

1. Processing of Cytokines, Chemokines, and Growth Factors. TNF- α and IL-1 β are inflammatory cytokines synthesized as inactive membrane-bound pro-forms and are converted to their active forms by the metalloprotease TNF- α converting enzyme (Black et al., 1997) and by the cysteine protease IL-1 β -converting enzyme (caspase-1) (Black et al., 1988; Weber et al., 2010), respectively. PR3, however, can also cleave the proforms of TNF- α and IL-1 β at Val-Arg bonds (Robache-Gallea et al., 1995; Coeshott et al., 1999). The effect of HNE on the processing of TNF- α is not clear; some studies claim that HNE degrades pro-TNF- α with a loss of activity; others suggest that HNE liberates soluble, biologically active TNF- α from its membrane-bound precursor. We showed that a synthetic FRET substrate derived from the pro-TNF- α sequence is efficiently cleaved by PR3 and HNE (Korkmaz et al., 2007). PR3, but not HNE, activates IL-1 β . This is most probably due to a negatively charged residue at the P4 and a positively charged residue at the P1' position in pro-IL-1 β that electrostatically could interact with Lys99 and Asp 61 of the active-site region of PR3 but not with HNE (Korkmaz et al., 2007).

The pro-inflammatory cytokine IL-18 belongs to the IL-1 cytokine family and is an important regulator of the innate and acquired immune response. It is synthesized as an inactive precursor and can be processed by caspase-1, caspase-3, and PR3 to its active form, but only the caspase-1 and caspase-3 cleavage sites have been identified (Akita et al., 1997). By contrast to HNE, PR3 could cleave caspase 3 substrates because of its preference of aspartyl residues at P2 and P2' (Korkmaz et al., 2007, 2008c). Caspase 3 cleaves after an Asp residue if another Asp is present at the P4 position (Stennicke et al., 2000; Wei et al., 2000). Thus, PR3 can cleave caspase-3 substrates two residues upstream of the caspase-3 cleavage site if the P2 position of a caspase 3 substrate is compatible with the S1 subsite of PR3. Based on this analysis, the predicted PR3 cleavage site in the pro-IL18 would be at the C-R bond in the -MTD⁷¹SDC↓RD⁷⁶NA- sequence, whereas that of caspase 3 has been identified after Asp76.

IL-8 is a major chemokine responsible for neutrophil degranulation and neutrophil migration to inflammatory sites (Baggiolini and Clark-Lewis, 1992; Baggiolini et al., 1994). It is secreted as a precursor by neutrophils, monocytes, endothelial cells, and fibroblasts in response to inflammatory stimuli. Full-length pro-IL-8 (77 residues) is converted by MMP-8, MMP-9, and PR3 to three truncated variants (70, 71, and 72 residues long) retaining chemotactic activity in human granulocyte lysates (Padrines et al., 1994; Van den Steen et al., 2000). PR3 (but also lysates of neutrophil granules) cleaves the full-length pro-IL-8 at the Ala-Lys bond (-AVLPRSA²⁹ ↓ **KEL**-), liberating the most active form of IL-8 (IL-70). The FRET substrate derived from this sequence is cleaved by PR3 but not by HNE (B. Korkmaz, unpublished results). The Ser residue at P2 and positively and negatively charged residues at P1' and P2' (bold characters) explain the specific cleavage of pro-IL-8 by PR3.

The stromal cell-derived factor-1 α (SDF-1 α), also called CXCL12, is a chemokine constitutively produced by hematopoietic cells, but SDF-1 mRNA and protein have also been identified in the central nervous system in neuronal, astroglial, microglial, and endothelial cells. SDF-1 α plays a critical role in cell migration because it is a chemotactic factor for T cells, monocytes, pre-B cells, dendritic cells, and hematopoietic progenitor cells (Barbieri et al., 2007). Gene inactivation of SDF-1 α or of its receptor CXCR4 in mice impairs myelo- and lymphopoiesis (Ma et al., 1998; Odemis et al., 2005). In vitro, HNE and CG, but not PR3, process the highly flexible N-terminal end of SDF-1 α , which results in decreased activity. Processing by HNE releases the N-terminal tripeptide Lys1-Pro2-Val3 (Valenzuela-Fernández et al., 2002), whereas that by CG occurs at the Leu5-Ser6 bond, liberating a pentameric peptide (Delgado et al., 2001).

Progranulin, also called proepithelin, is a heavily glycosylated growth factor of 90 kDa, ubiquitously expressed and involved in tissue regeneration, tumorigenesis, and inflammation (Bateman and Bennett, 1998; Zhu et al., 2002). It is also produced and secreted into the extracellular environment by TNF- α -activated neutrophils. Progranulin inhibits adhesion-dependent neutrophil activation by interfering with the secretion of neutrophil proteases and the production of reactive oxygen species (Zhu et al., 2002), but the mechanisms involved in these anti-inflammatory effects are not yet elucidated. Anti-inflammatory properties of progranulin are suppressed through proteolytic cleavage by HNE and PR3 (Zhu et al., 2002; Kessenbrock et al., 2008). Interestingly enough, processed granulin peptides possess pro-inflammatory properties, stimulating IL-8 release from granulocytes (Zhu et al., 2002). In a recent study, mice lacking both NE and PR3 showed a highly diminished, immune complex-mediated, neutrophil infiltration that was due to impaired progranulin degradation, thus emphasizing the crucial role of progranulin

as an inflammation-suppressing mediator (Kessenbrock et al., 2008).

2. *Processing and Activation of Cellular Receptors.* NSPs contribute to immune regulation also through the cleavage and activation of specific cellular receptors. HNE, PR3, and CG can process the N-terminal extracellular domains of protease-activated receptors (PARs), which are a subfamily of related G-protein-coupled receptors (Ossovskaya and Bunnett, 2004; Vergnolle, 2009). These receptors are ubiquitously expressed in various tissues and cells and, more especially, in platelets and endothelial cells. Processing of PAR extracellular domains occurs through exposure of a tethered ligand that allows the autoactivation of the receptor and subsequent activation of an intracellular signaling cascade via phospholipase C (Ossovskaya and Bunnett, 2004; Vergnolle, 2009). Four PARs have been identified so far; three of them, PAR-1, PAR-3, and PAR-4, can be activated by thrombin. Besides thrombin, CG released from activated neutrophils can also activate PAR-4 at the surface of platelets and initiate their aggregation (Sambrano et al., 2000). All three NSPs cleave PAR-1, which impairs their activation by thrombin (Renesto et al., 1997). The sequence containing the CG cleavage site (-EPF⁵⁵ ↓ WEDEE-) (Renesto et al., 1997) has been used to raise a sensitive FRET substrate for this protease (Attucci et al., 2002). PAR-2 is expressed on endothelial cells and can be activated by trypsin (SKGR³⁴ ↓ SLIGKV) (Nystedt et al., 1994, 1995a,b) but also by the three NSPs (Uehara et al., 2002, 2003, 2004). PAR-2 activation results in the production and secretion of IL-8 and chemokine (C-C motif) ligand 2 (Uehara et al., 2003, 2004).

Toll-like receptors (TLRs) are transmembrane glycoproteins remarkably contributing to host defense against microbial infections and innate immune response. Thirteen mammalian TLRs have been identified so far. Most of them can recognize specific pathogen-associated molecular patterns presented by invading pathogens or danger-associated molecular patterns released by injured tissues (Akira et al., 2006; Creagh and O'Neill, 2006; Brikos and O'Neill, 2008; Buchanan et al., 2009). The LPS-sensitive TLR4 and EGFR can be directly up-regulated by HNE in lung epithelial cells, which results ultimately in an overproduction of pro-IL-8 mediated through the Myd88/IRAK/TRAF-6 pathway (Walsh et al., 2001; Devaney et al., 2003; Bergin et al., 2008). This HNE effect can be reduced by the addition of the serine protease inhibitor phenylmethylsulfonyl fluoride (Devaney et al., 2003). A new mechanism of HNE-induced pro-IL-8 expression involving activation of the metalloprotease meprin α has been identified (Bergin et al., 2008).

Receptors for the Fc region of IgG and integrin CD11b/CD18 at the neutrophil surface are involved in the recognition of immune complexes, which results in neutrophil activation through modulation of integrin clustering at the cell surface, cytoskeletal rearrangement, and intracellular ROS production (Raptis and Pham, 2005).

CG could enhance immune complex-receptor-mediated neutrophil activation as demonstrated using CG/NE double-deficient mice (Raptis et al., 2005), but the relevant CG target has not yet been identified.

3. *Induction of Apoptosis by Proteinase 3.* PR3 secreted by activated neutrophils during inflammation is involved in endothelial cell apoptosis (Yang et al., 2001; Preston et al., 2002; Pendergraft et al., 2004). The mechanism by which neutrophil-secreted PR3 enters the endothelial cell has not been elucidated but its molecular intracellular targets have been clearly identified. PR3 directly processes NF κ B at the Cys-Arg bond in the sequence -KDC⁹⁵↓RDGA- (Preston et al., 2002) and the cyclin-dependent kinase inhibitor p21 at the Ala-Arg bond in the sequence -IQEA⁴⁵↓RER- (Dublet et al., 2005) (Fig. 5B). The proteolytic processing of NF κ B and of p21 accelerates endothelial cell apoptosis. Apoptotic elimination of cells from inflammatory sites helps to resolve inflammation. As reported above for pro-IL-18, the positioning of the two Asp residues in the cleaved sequence of NF κ B indicates that caspase 3 also cleaves this sequence but at a different site, located two residues downstream from the PR3 cleavage site. No preferential HNE cleavage site is present in this sequence, which explains the specific proapoptotic properties of PR3. The mouse homolog of human PR3, however, has a different specificity that impairs the cleavage of NF κ B and p21 at the same sites (Kalupov et al., 2009) (Fig. 5B). Because human and mouse p21 and NF κ B share the same sequence in this region, it is questionable whether these antiapoptotic properties of PR3 are biologically relevant.

Many other molecular targets of NSPs have been identified as membrane-bound and soluble substrates at inflammatory sites (for review, see Bank and Ansoorge, 2001; Wiedow and Meyer-Hoffert, 2005; Pham, 2006, 2008; Meyer-Hoffert, 2009), and many others probably remain to be discovered. Proteolytic cleavage of these molecular targets may result in the activation of latent proforms, in the enhancement or abolishment of pre-existing activities, or in anticipated degradation of inactive proforms that impair interaction with their physiological activators.

IV. Physiological Inhibitors of Elastase, Proteinase 3, and Cathepsin G

During phagocytosis and neutrophil turnover, HNE, PR3, and CG are released into the extracellular space as active proteases. The proteolytic activity of HNE, PR3, and CG seems to be tightly regulated in the extracellular and pericellular space to avoid degradation of connective tissue proteins including elastin, collagen, and proteoglycans (Janoff, 1985). Protein inhibitors that belong to three main families, the serpins, the chelonianins, and the macroglobulins, ultimately control proteolytic activity of HNE, PR3, and CG activities. The individual contributions of these families depend on their tissue localization and that of their target proteases. The main characteristics of HNE, PR3, and CG physiological inhibitors are presented in Table 2.

A. Serine Protease Inhibitors

Serpins are the largest and most diverse family of protease inhibitors; more than 1000 members have been identified in human, plant, fungi, bacteria, archaea, and certain viruses (Silverman et al., 2001; Mangan et al., 2008). They share a similar highly conserved tertiary structure and similar molecular weight of approximately 50 kDa. Human serpins belong to the first nine clades (A–I) of the 16 that have been described based on phylogenetic relationships (Irving et al., 2000; Silverman et al., 2001; Mangan et al., 2008). For historical reasons, α 1-protease inhibitor (α 1-PI) was assigned to the first clade. Clade B, also known as the ov-serpin clan because of the similarity of its members to ovalbumin (a protein that belongs to the serpin family but lacks inhibitory activity), is the second largest clan in humans, with 15 members identified so far. Ov-serpin clan members are generally located in the cytoplasm and, to a lesser extent, on the cell surface and nucleus (Remold-O'Donnell, 1993).

Serpins play important regulatory functions in intracellular and extracellular proteolytic events, including blood coagulation, complement activation, fibrinolysis, cell migration, angiogenesis, and apoptosis (Potempa et al., 1994). Serpin dysfunction is known to contribute to

TABLE 2
Main characteristics of the endogenous inhibitors of elastase, proteinase 3, and cathepsin G

	Reactive site	Target Proteases	Source
Serpin			
α 1-PI	Met358–Ser359	Elastase, proteinase 3, cathepsin G, trypsin, plasmin, thrombin, chymotrypsin	Plasma, neutrophil
ACT	Leu358–Ser359	Cathepsin G, chymase, chymotrypsin	Plasma
MNEI	Phe343–Cys344	Cathepsin G, chymase, kallikrein 3	Neutrophil, macrophage
	Cys344–Met345	Elastase, proteinase 3	
PI6	Arg341–Cys342	Cathepsin G	Placenta, granulocytes
PI9	Glu340–Cys341	Granzyme B, caspase 1	Lymphocyte T cells
	Cys341–Cys342	Elastase	Endothelial cells, epithelial cells
Chelonianin			
SLPI	Leu72–Met73	Elastase, cathepsin G, chymase, chymotrypsin	Epithelial cells, seminal plasma, neutrophil, macrophage
Elafin	Ala24–Met25	Elastase, proteinase 3	Bronchial secretions, skin, seminal plasma

diseases such as emphysema, thrombosis, angioedema, and cancer (Carrell and Lomas, 1997; Lomas and Carrell, 2002). Most inhibitory serpins target trypsin-/chymotrypsin-like serine proteases, but some, termed "cross-class inhibitors," have been shown to target cysteine proteases (Annand et al., 1999). The crystal structure of the prototype plasma inhibitor α 1-PI revealed the archetype native serpin fold (Loebermann et al., 1984). All serpins typically have three β -sheets (termed A, B, and C) and eight or nine α -helices (hA–hI) arranged in a stressed configuration. The so-called reactive center loop (RCL) of inhibitory molecules determines specificity and forms the initial encounter complex with the target protease (Potempa et al., 1994; Silverman et al., 2001). Serpins inhibit proteases by a suicide substrate inhibition mechanism. The protease initially recognizes the serpin as a potential substrate using residues of the reactive center loop and cleaves it between P1 and P1'. This cleavage allows insertion of the cleaved RCL into the β -sheet A of the serpin, dragging the protease with it and moving it over 71 Å to the distal end of the serpin to form a 1:1 stoichiometric covalent inhibitory complex (Huntington et al., 2000). Such cleavage generates a ~4-kDa C-terminal fragment that remains noncovalently bound to the cleaved serpin. Displacement of the covalently attached active site serine residue from its catalytic partner histidine explains the loss of catalytic function in the covalent complex. The distortion of the catalytic site structure prevents the release of the protease from the complex, and the structural disorder induces its proteolytic inactivation (Huntington et al., 2000). Covalent complex formation between serpin and serine proteases triggers a number of conformational changes, particularly in the activation domain loops of the bound protease (Dementiev et al., 2006).

1. α 1-Protease Inhibitor. α 1-PI is a single-chain glycoprotein of 394 amino acids synthesized mainly by hepatocytes; it was originally named α 1-antitrypsin because of its ability to irreversibly bind trypsin in vitro (Janciauskiene, 2001). It is the most abundant serpin present in human blood. Its primary function, however, seems to be in the lung parenchyma, where it protects alveolar tissues from destruction by NSPs. Its circulating level lies between 1.2 and 2 mg/ml in healthy persons (Jeppsson et al., 1978; Crystal et al., 1989), but it may increase during acute phases of inflammation and infection. The gene is located on the long arm of chromosome fourteen (14q32.1). More than 100 different genetically encoded variants of α 1-PI have been described. At the protein level, α 1-PI variants have been discriminated by isoelectric focusing (Hutchison, 1988) and are designated by a capital letter corresponding to their isoelectric point. The most common variant is the M type. Abnormalities of the S and Z types arise from single amino acid substitutions in the primary chain and result in decreased or undetectable α 1-PI levels in serum (Hutchison, 1988). The crystal structure of α 1-PI obeys

the general structure of serpins with an exposed RCL that is cleaved at the Met358–Ser359 bond upon interaction with the target protease (Huntington et al., 2000). α 1-PI is an excellent irreversible inhibitor of HNE that also inhibits related neutrophil proteases PR3 and CG. α 1-PI inhibits HNE with an inhibitor/enzyme stoichiometry of 1, whereas that with PR3 and CG is slightly higher because of partial proteolytic inactivation of some inhibitor molecules occurring during the course of the interaction (Duranton and Bieth, 2003; Korkmaz et al., 2005b). The second-order constants of association of α 1-PI with HNE, PR3, and CG are 6.5×10^7 , 8.1×10^6 , and $4.1 \times 10^5 \text{ M}^{-1} \cdot \text{s}^{-1}$, respectively (Beatty et al., 1980; Rao et al., 1991). Neutrophil membrane-bound HNE and PR3 are also inhibited by α 1-PI to form soluble irreversible complexes (Korkmaz et al., 2005a, 2009). Conformational distortion of the hydrophobic 217–225 loop of PR3 involved in membrane interaction most likely triggers solubilization of mPR3 (Korkmaz et al., 2008b).

The association of α 1-PI with target proteases is altered by their interaction with DNA, heparin, and other glycosaminoglycans found at inflammatory sites (Frommherz and Bieth, 1991; Frommherz et al., 1991; Bologey and Bieth, 1998; Ying and Simon, 2000). Heparin promotes the formation of the Michaelis complex between HNE and α 1-PI but prevents conversion into a covalently inactivated complex (Faller et al., 1993). DNA and heparin also decrease the rate constant of association between CG and α 1-PI (Ermolieff et al., 1994; Duranton et al., 2000). The conformational change of α 1-PI induced by complexation with a protease results in the appearance of new binding sites that are recognized by serpin-enzyme complex surface receptors (Perlmutter et al., 1990) or by receptors for low- and very low-density lipoproteins (Kounnas et al., 1996; Rodenburg et al., 1998), which allows for their clearance.

Proteolytic cleavage of the α 1-PI reactive loop by exogenous or endogenous proteases and/or oxidation by biological oxidants of methionine residues in this loop alters its biological activity. MMP-8 (Knäuper et al., 1990; Michaelis et al., 1990), MMP-9 (Desrochers et al., 1992), leukolysine (Nie and Pei, 2004), MMP-7 (Zhang et al., 1994), cathepsin L (Johnson et al., 1986), and bacterial proteases produced by *Staphylococcus aureus*, *Serratia marcescens* (Rapala-Kozik et al., 1999), and *Pseudomonas aeruginosa* (Moriyama et al., 1984) count among the proteases degrading α 1-PI. RCL cleavages generate a ~4-kDa fragment similar to that generated by target proteases (Banda et al., 1988a). α 1-PI contains 10 methionine residues (Vogt, 1995). Oxidation of two of them, Met358 and Met351, results in a marked loss of affinity of α 1-PI for HNE and CG (Johnson and Travis, 1979; Beatty et al., 1980; Taggart et al., 2000). Oxidation of α 1-PI is observed in vitro upon incubation with myeloperoxidase or activated neutrophils (Shock and Baum, 1988; Padrines and Bieth, 1993).

2. *α 1-Antichymotrypsin.* α 1-Antichymotrypsin (ACT) is a plasma glycoprotein synthesized by hepatocytes and secreted into the serum. Its serum concentration of approximately 0.25 mg/ml increases during acute inflammation by almost 5-fold (Calvin and Price, 1986). ACT contains 400 amino acids and has two glycosylation sites on Asn70 and Asn104, carbohydrate groups at these positions accounting for approximately 25% of the protein's mass. It displays a relatively high sequence identity with α 1-PI (45%), suggesting that both inhibitors have evolved through duplication of a single gene (Bao et al., 1987). ACT can bind double-stranded DNA through several lysyl residues (Naidoo et al., 1995), a feature thought to be of relevance in controlling tumor progression of the thyroid gland (Lai et al., 1998). ACT is also recognized as a major constituent of amyloid deposits in the brains of patients with Alzheimer disease (Abraham et al., 1988).

ACT inhibits serine proteases of the chymotrypsin type. The main targets of ACT are CG ($k_{\text{ass}} = 5.1 \times 10^7 \text{ M}^{-1} \cdot \text{s}^{-1}$), chymotrypsin, and mast cell chymase (Travis et al., 1978; Fukusen et al., 1987), with which it forms a covalent complex after cleavage of its inhibitory loop. The reactive site of ACT has been identified at the Leu358–Ser359 bond. ACT does not inhibit HNE and PR3 but is proteolytically degraded by HNE (Rubin et al., 1994). Neutrophil MMP-8 but not MMP-9 inactivates ACT by cleaving the inhibitory loop at the Ala362–Leu363 bond (Desrochers et al., 1992). Several other MMPs, including MMP-1 and MMP-2 (Mast et al., 1991), and bacterial proteases can inactivate ACT by cleaving its reactive center loop (Kress, 1983).

3. *Monocyte Neutrophil Elastase Inhibitor, Proteinase Inhibitor 6, and Proteinase Inhibitor 9.* Monocyte neutrophil elastase inhibitor (MNEI, now called SerpinB1), PI6, and PI9 are three cytoplasmic and/or nuclear serpins that belong to the family of ovalbumin and are potential inhibitors of one or more NSPs. The gene encoding serpinB1 (Zeng et al., 1998) is located on chromosome 6 in a cluster with those encoding PI6 and PI9 (Sun et al., 1998). SerpinB1 was first identified as a potent inhibitor of HNE present in the cytoplasm of neutrophils and monocytes (Remold-O'Donnell et al., 1989, 1992). Recombinant serpinB1 inhibits HNE ($k_{\text{ass}} = 3.4 \times 10^7 \text{ M}^{-1} \cdot \text{s}^{-1}$), PR3 ($k_{\text{ass}} = 1.7 \times 10^7 \text{ M}^{-1} \cdot \text{s}^{-1}$), and porcine pancreatic elastase but also chymotrypsin-like proteases [e.g., CG ($k_{\text{ass}} = 2.3 \times 10^6 \text{ M}^{-1} \cdot \text{s}^{-1}$) and chymase] with a stoichiometry of inhibition close to 1 (Cooley et al., 2001). This duality is explained by the presence of two functional sites in the reactive center loop, one at Phe343–Cys344, allowing interaction with chymotrypsin-like protease, and the other at Cys344–Met345, which is cleaved by elastase-related proteases (Cooley et al., 2001).

PI9, which shares 49% sequence identity with serpinB1, is present in placenta, endothelial cells, and in lung (Sprecher et al., 1995; Buzza et al., 2001). PI9 protects host cells from apoptosis by inhibiting gran-

zyme B (Sun et al., 1996). It also inhibits the cysteine protease caspase-1, which catalyzes the formation of interleukin-1 β from its precursor (Annand et al., 1999). PI9 is the first example of a human serpin that can inhibit a cysteine protease. It also inhibits bacterial proteases and subtilisin A (Dahlen et al., 1997), and its recombinant form inhibits HNE with $k_{\text{ass}} = 1.5 \times 10^5 \text{ M}^{-1} \cdot \text{s}^{-1}$ (Dahlen et al., 1999). The inhibition of HNE occurs through cleavage of the Cys341–Cys342 bond in the PI9-reactive loop.

PI6 was identified in 1993 as an inhibitor of trypsin, urokinase plasminogen activator, and plasmin (Coughlin et al., 1993) but has also been found in monocytes in a complex with CG (Scott et al., 1999). Cytoplasmic inhibition of CG may protect these cells against damage during biosynthesis. The relevance of this reaction is supported by the high rate constant for association with CG ($k_{\text{ass}} = 6.8 \times 10^6 \text{ M}^{-1} \cdot \text{s}^{-1}$), (Scott et al., 1999).

B. Canonical Inhibitors

Canonical inhibitors include a still increasing number of families with different folds but sharing a canonical conformation of their inhibitory protease binding loop in the P3-P3' region (Bode and Huber, 1992). This loop is a convex, extended, and solvent-exposed structure that is highly complementary to the concave active site of the enzyme. A huge number of canonical inhibitors have been isolated from various cells, tissues, and organisms, including plant seeds, avian eggs, and various body fluids (Krowarsch et al., 2003). The chelonianin family of canonical inhibitors includes the physiological endogenous inhibitors of NSPs, SLPI, elafin, and its precursor trappin-2 (Moreau et al., 2008).

1. *Secretory Leukocyte Protease Inhibitor.* SLPI is an 11.7-kDa nonglycosylated highly basic (pI > 11) protein consisting of 107 amino acids found in all body fluids, including tears, salivary glands, seminal fluid, bronchial secretions, cervical, and intestinal mucus (Si-Tahar et al., 2000; Doumas et al., 2005). Its wide distribution in the body explains why it was given different names: "bronchial inhibitor," "human seminal plasma inhibitor," "anti-LeukoProtease," "mucus protease inhibitor," and SLPI. In the lung, it is produced by epithelial cells of the trachea and bronchi, by alveolar type II cells, and by tracheal gland serous cells and Clara cells (Sallenave et al., 1997a; Sallenave, 2002). SLPI is present at highest concentrations in the upper airways. In the deep lung, SLPI concentration is low but it could play a physiological role, because it has been demonstrated by immunohistochemistry to be in contact with elastin fibers (Kramps et al., 1989). SLPI is also synthesized by phagocytes (neutrophils, monocytes, and alveolar macrophages) (Sallenave et al., 1997b). Its crystal structure obtained as a complex with bovine chymotrypsin shows two domains of similar architecture, each stabilized by four disulfide bridges (Grütter et al., 1988) but only the C-terminal domain is complexed to chymotrypsin.

SLPI is a reversible inhibitor of HNE [$k_{\text{ass}} = 6.4 \times 10^6 \text{ M}^{-1} \cdot \text{s}^{-1}$ (Boudier and Bieth, 1989), $K_i = 0.1 \times 10^{-10} \text{ M}$ (Gauthier et al., 1982)], CG [$k_{\text{ass}} = 1.5 \times 10^6 \text{ M}^{-1} \cdot \text{s}^{-1}$ (Fath et al., 1998), $K_i = 4.2 \times 10^{-9} \text{ M}$ (Smith and Johnson, 1985)], chymotrypsin, chymase, and bovine trypsin, but it does not inhibit PR3. Its reactive site extends on each side of the Leu72–Met73 bond located in its C-terminal domain. Heparin binding to SLPI induces a conformational change that accelerates inhibition of HNE (Faller et al., 1992). Fragments of native heparin (4.5 or 8.1 kDa) or *O*-butyryl (8 kDa) also accelerate the inhibition of CG by SLPI (Ermolieff et al., 1998).

Recently, a C-terminal domain of SLPI has been crystallized in a complex with HNE. X-ray data showed the importance of P1 Leu72 and of six hydrogen bonds in the primary contact region for inhibiting HNE and of P5 Tyr68, which forms a hydrogen bond with Arg217 of HNE for increasing the selectivity of SLPI toward this protease (Koizumi et al., 2008). The lack of PR3 inhibition by SLPI is explained by the presence of Ile190 (Val in HNE), which reduces the size of the S1 pocket of PR3, thus impairing accommodation of P1 Leu72 of the inhibitor (Fujinaga et al., 1996), and by the lack of a hydrogen bond between Tyr68 and Arg217 due to substitution of Arg217 by an Ile in the S5 pocket of PR3 (Koizumi et al., 2008). The unfavorable positive-positive contacts between PR3 and SLPI at two locations, one involving Arg36/Arg65 and the other Arg168/Lys99 of PR3, contribute also to the noninhibition of PR3 by SLPI (Zani et al., 2009).

Oxidation of Met73 in the SLPI inhibitory loop decreases the association rate constant for HNE by a factor of 20 (Boudier and Bieth, 1994), suggesting that the efficacy of the inhibitor is less affected by oxidation than that of α 1-PI. The N-terminal domain of SLPI stabilizes the inhibitor thus favoring trypsin inhibition. This domain is also essential for activation of the inhibitor by heparin (Faller et al., 1992). Bacterial proteases and human cysteine proteases (cathepsin B, L, and S) can inactivate SLPI by proteolytic degradation (Sponer et al., 1991; Draper et al., 1998; Taggart et al., 2001). Unlike α 1-PI, SLPI is able to inhibit HNE in vitro when linked to its natural substrate elastin (Hornebeck and Schnebli, 1982; Bruch and Bieth, 1986). Because of its lower molecular weight compared with α 1-PI, SLPI can access the space between adherent neutrophil and extracellular matrix, thus protecting extracellular matrix proteins from proteolysis (Rice and Weiss, 1990).

2. Elafin. Elafin is a nonglycosylated 6-kDa inhibitor also called “skin-derived anti-leuko-protease” or “elastase specific inhibitor.” Elafin was originally isolated from the skin of patients affected by psoriasis (Schalkwijk et al., 1990; Wiedow et al., 1990) but it is also present in lung secretions (Sallenave and Ryle, 1991). As with SLPI, it has a tracheobronchial origin, being synthesized by Clara cells and type II pneumonocytes (Sallenave, 2002).

Elafin is a basic inhibitor with a pI of 9.7, and it is stable at acidic pH (Wiedow et al., 1990). Its three-dimensional structure has been determined by solving the structure of a complex with porcine pancreatic elastase (Tsunemi et al., 1996). Similar to SLPI, it displays a compact structure maintained by four disulfide bridges, characteristic of whey acidic proteins. Elafin shares 40% of sequence identity with SLPI, and the active site residues are also similar. Elafin is released by proteolytic processing from a larger precursor made of two functional domains called trappin-2 or pre-elafin (Schalkwijk et al., 1999). The N-terminal domain of trappin-2 contains a repeated sequence GQDPVK acting as a transglutaminase substrate and therefore allows adsorption of the inhibitor on extracellular matrix proteins by interstitial transglutamination (Schalkwijk et al., 1999). Trappin immobilization could help maintain local inhibition compared with other soluble inhibitors of NSPs.

Elafin is a potent inhibitor of both HNE [$k_{\text{ass}} = 5 \times 10^6 \text{ M}^{-1} \cdot \text{s}^{-1}$ (Ying and Simon, 2001), $K_i = 0.8 \times 10^{-10} \text{ M}$ (Zani et al., 2004)] and PR3 [$k_{\text{ass}} = 4 \times 10^6 \text{ M}^{-1} \cdot \text{s}^{-1}$ (Ying and Simon, 2001), $K_i = 1.2 \times 10^{-10} \text{ M}$ (Zani et al., 2004)] but, unlike SLPI, does not inhibit CG. Elafin interacts with HNE and PR3 through its active site centered on the Ala24–Met25 peptide bond. The presence of an Ala residue at P1 is consistent with its specificity toward PR3 and HNE. Elafin/trappin-2 can also inhibit HNE and PR3 at the surface of activated neutrophils (Zani et al., 2009). Whereas membrane-associated HNE forms soluble complexes upon interaction with elafin, mPR3 complexes remain on the neutrophil surface, which indicates that HNE and PR3 are differently bound to neutrophil surfaces (Korkmaz et al., 2009). A recent in vitro study demonstrated that an excess of HNE at Val5 and Val9 cleaves recombinant elafin at Val5 and Val9. This does not affect its capacity to inhibit HNE but strongly impairs its ability to bind LPS and its immobilization by transglutamination (Guyot et al., 2008). This could greatly weaken its contribution to the defense of invading pathogens (Sallenave, 2002; Moreau et al., 2008).

C. α -Macroglobulins

Human α 2-macroglobulin is a polyvalent homotetrameric inhibitor of 725 kDa present at a concentration of 2 mg/ml in serum (Petersen, 1993). It inhibits all classes of proteases, including NSPs (Travis, 1988). Because its high molecular mass impairs diffusion to inflammatory sites during neutrophil extravasation, its major role is probably restricted to controlling protease activity within the circulation. Its mechanism of interaction with proteases has been described in detail (Sottrup-Jensen, 1989). Its covalent association with proteases sterically shields their active sites from large molecular substrates, hence permitting enzymatic hy-

drolysis of only small synthetic substrates (Doan and Gettins, 2007).

V. Pathophysiology of Elastase, Proteinase 3 and Cathepsin G in Human Diseases

A. Chronic Inflammatory Lung Diseases

In many instances, the initiation and propagation of lung damage is a consequence of an exaggerated inappropriate inflammatory response, which includes the release of proteases and leukocyte-derived cytotoxic products (Owen, 2008b; Roghanian and Sallenave, 2008). Inflammation is a physiological protective response to injury or infection consisting of endothelial activation, leukocyte recruitment and activation, vasodilation, and increased vascular permeability. Although designed to curtail tissue injury and facilitate repair, the inflammatory response sometimes results in further injury and organ dysfunction. Inflammatory chronic lung diseases, chronic obstructive pulmonary disease, acute lung injury, acute respiratory distress syndrome, and cystic fibrosis are syndromes of severe pulmonary dysfunction resulting from a massive inflammatory response and affecting millions of people worldwide. The histological hallmark of these chronic inflammatory lung diseases is the accumulation of neutrophils in the microvasculature of the lung. Neutrophils are crucial to the innate immune response, and their activation leads to the release of multiple cytotoxic products, including reactive oxygen species and proteases (serine, cysteine, and metalloproteases). The physiological balance between proteases and antiproteases is required for the maintenance of the lung's connective tissue, and an imbalance in favor of proteases results in lung injury (Umeki et al., 1988; Tetley, 1993). A number of studies in animal and cell culture models have demonstrated a contribution of HNE and related NSPs to the development of chronic inflammatory lung diseases. Available preclinical and clinical data suggest that inhibition of NSP in lung diseases suppresses or attenuates the contribution of NSP to pathogenesis (Chughtai and O'Riordan, 2004; Voynow et al., 2008; Quinn et al., 2010). HNE could also participate in fibrotic lung remodeling by playing a focused role in the conversion of latent transforming growth factor- β into its biologically active form (Chua and Laurent, 2006; Lungarella et al., 2008).

1. Chronic Obstructive Pulmonary Disease. Chronic obstructive pulmonary disease (COPD) represents a group of diseases, including chronic bronchitis and emphysema, that are characterized by an airflow limitation that is not fully reversible (Barnes and Stockley, 2005). COPD represents an increasingly important cause of morbidity and mortality in the population. It is the fifth leading cause of death in the world, is expected to rise to third place by 2020, and is most often due to tobacco smoking or exposure to other airborne irritants or solvents, which trigger an abnormal inflammatory re-

sponse in the lung. It is characterized by an increased number of neutrophils, macrophages, and T lymphocytes predominantly localizing in small airways and lung parenchyma (Barnes and Stockley, 2005; Owen, 2008b). One genetic cause of COPD, accounting for approximately 2% of cases, is α 1-PI deficiency (Laurell and Eriksson, 1963), which is associated with the Z phenotype. In patients with α 1-PI deficiency, the development of COPD is believed to be caused by the uncontrolled action of proteases on lung tissue. Intermittent infusions of active plasma-derived α 1-PI in these patients increased the levels of α 1-PI and anti-HNE capacities for a few days after infusion (Wewers et al., 1987). In smokers with emphysema, extracellular matrix undergoes significant physical and biochemical modifications. COPD is initiated by cigarette smoke or other irritants that activate respiratory tract macrophages (Barnes, 2004), which release neutrophil chemotactic factors, including IL-8 and leukotriene B₄, that induce neutrophil infiltration/accumulation in the lung and subsequent secretion of active NSPs (Barnes, 2004). Indeed, an increased level of NSP is observed in bronchoalveolar lavage (BAL) fluids of patients with COPD. The pathogenic roles of NSPs in COPD are attributed to their ability to break down connective tissue components and generate proinflammatory peptides from these components (Houghton et al., 2006; Weathington et al., 2006), to induce mucus secretion by submucosal glandular cells and goblet cells, and to express proinflammatory cytokines from airway epithelial cells (Sommerhoff et al., 1990; Takeyama et al., 1998; Witko-Sarsat et al., 1999b). It should be emphasized that NSPs are not the only proteases participating in lung damage in COPD; the role of other granular serine proteases, including MMPs, A disintegrin and metalloproteases, and cysteine proteases, has been reviewed recently by Owen (2008b).

Studies in animal models have shown that an imbalance between proteases and antiproteases in the lung favors increased proteolysis, thus contributing to COPD pathogenesis (Stockley, 1999; Barnes and Stockley, 2005; Owen, 2008b). An imbalance between oxidants and protective antioxidants resulting in oxidative stress could also contribute to COPD pathogenesis (Wood and Stockley, 2006). This is supported by the observation that oxidized, inactive α 1-PI is present in BAL of smokers suffering from emphysema (Morrison et al., 1986a,b, 1987; Sethi and Rochester, 2000). Oxidation of α 1-PI Met residues to Met-sulfoxides inactivates the inhibitor as shown by the analysis of BAL from smokers compared with nonsmokers (Gadek et al., 1979; Carp et al., 1982). Oxidation, however, cannot be responsible for the inactivation of ACT in BAL of patients with COPD. On the other hand, genetic alterations in the ACT gene are rare but have been reported. A single natural L55P substitution, for example, yields an ACT variant with little activity. Partial insertion of the reactive center loop into the β -sheet A (Chang and Lomas, 1998; Gooptu et al.,

2000) accounts for its dysfunction. BALs from COPD patients also contain oxidized SLPI and proteolytically processed fragments.

Experimental models have been developed to mimic human COPD (e.g., mouse) and use different injurious stimuli (e.g., cigarette smoke, instilled exogenous proteases) (Brusselle et al., 2006). In the mouse model of COPD, aerosolized human α 1-PI, serpinB1, SLPI, reduced the severity and the extent of the elastase-induced tissue damages and airspace enlargement (Rees et al., 1999; Churg et al., 2003; Pemberton et al., 2006). We recently showed, however, a limitation of the mouse model by demonstrating the different substrate specificities of mouse and human HNE and PR3 (Kalupov et al., 2009). This would certainly impair testing human NSP inhibitors of putative therapeutic interest in the mouse model because of their different reactivity with target proteases in these two species (Wiesner et al., 2005).

2. Cystic Fibrosis. Cystic fibrosis (CF; MIM 219700) is an inherited complicated disease of the secretory glands, originally described in 1938 by Dorothy H. Andersen (Davis, 2006). It has an estimated prevalence of 1 in 2500 in Europe and the United States (Tizzano and Buchwald, 1992). It affects the lungs, pancreas, liver, intestines, sinuses, and reproductive system (Voynow et al., 2008). CF is caused by a mutation in a gene named cystic fibrosis transmembrane conductance regulator (CFTR) (Riordan et al., 1989). The product of this gene is a chloride ion channel involved in the movement of chloride ions out of epithelial cells toward the covering mucus (Riordan et al., 1989; Buchanan et al., 2009). The flow of chloride ions helps to control the movement of water in tissues, which is necessary for the production of thin, freely flowing mucus. As a consequence of CFTR mutations, cells that line the airways, pancreas, and other organs produce unusually thick and sticky mucus (Buchanan et al., 2009). Mucus clogging the airways and glands leads to the characteristic signs and symptoms of cystic fibrosis.

Excessive mucus production is frequently associated with bacterial lung infection, mainly by *S. aureus* and *P. aeruginosa* (Buchanan et al., 2009). The host system responds vigorously. The inflammatory process in CF airways is characterized by a massive influx of neutrophils, representing 95% of the cell population in BAL. High levels of elastinolytic activity are thus detected in sputum and BAL from patients with CF (Fick et al., 1984; Jackson et al., 1984; Suter et al., 1984; Bruce et al., 1985). The concentration of active NSPs in the sputum determined using specific and sensitive FRET substrate varies from 10^{-9} to 10^{-7} M (A. Gauthier, unpublished data) and overwhelms that of inhibitors found locally. In addition to their direct proteolytic action on the pulmonary matrix, airway NSPs stimulate massive neutrophil accumulation via secretion of the potent neutrophil chemoattractant IL-8 from airway epithelial cells and by interfering with mucus production. NSPs also induce detachment of the ciliated cells from their

neighbors, causing epithelial disruption and impairing mucociliary clearance (Amitani et al., 1991).

In CF, the major lung problems are bacterial infections, inflammation, and airway obstruction (Amin and Ratjen, 2008), which occur despite the presence in CF lungs of cationic antimicrobial peptides such as lactoferrin, SLPI, lysozyme, defensins, and LL-37 (Rogan et al., 2006). Inactivation of LL-37 in CF sputum might contribute to the persistent susceptibility of CF patients to microbial colonization and infection. LL-37 inactivation in CF BAL is due to its association with glycosaminoglycans (Bergsson et al., 2009), DNA and/or filamentous F-actin (Bucki et al., 2007). Hypertonic saline disrupts glycosaminoglycans–LL-37 complexes thus promoting antimicrobial effects (Bergsson et al., 2009) but free LL-37 is then degraded by HNE and cathepsin D (Bergsson et al., 2009). The large amounts of DNA released by lysed neutrophils in the respiratory tract of patients with CF in response to infection can be disrupted through therapeutic DNase administration, thus resulting in the liquefaction of viscous mucus, a reduction of the viscoelasticity of purulent lung secretions, an airflow increase, and a consequently decreased risk of infection (Fitzgerald et al., 2005). DNase increases the amount of LL-37 peptide detected in the supernatant of CF sputum dissolved from DNA/actin bundles (Bucki et al., 2007). It also increases proteolytic activity by releasing positively charged NSPs embedded in the DNA network. Combining factors that disrupt DNA and GAGs complexes with an anti-protease cocktail could potentially help promote antimicrobial and antiproteolytic activities in lung secretions of patients with CF. As detailed in a recent study (Griese et al., 2008), neutrophils from patients with CF, COPD, or bronchiectasis are ineffective in eliminating bacteria and have poor bacteriocidal killing capacity. Reduction of CXCR1 on the patients' neutrophils was observed and was shown to be linked to the action of HNE. The cleaved CXCR1 fragments in turn were able to activate the epithelial TLR2 and to induce local IL-8 production (Hartl et al., 2007). The chemokine IL-8 is known to be critically involved in the recruitment of neutrophils to the lungs and is increased in all conditions of persistent neutrophilic airway inflammation. Neutrophils treated with IL-8 or TLR2 agonist release pro-MMP-9, which can be activated by plasmin or other proteases. Pericellular MMP-9 inactivates α 1-PI and generates an inhibitor-free environment for HNE and PR3. PR3 in turn is able to remove an N-terminal heptapeptide from full-length IL-8 (residues 8–77 starting with KELRC) and enhances its agonist activity on CXCR2 in a positive feedback loop. Simultaneously, HNE can inactivate TIMP-1, an MMP-9 inhibitor (Itoh and Nagase, 1995), and further assists in this amplification cycle. In contrast to other pro-MMP-9–expressing cells, neutrophils externalize pro-MMP-9 without associated TIMP-1, which after activation in a TIMP-1–free environment can also cleave IL-8 but at a different site,

removing just six N-terminal residues (7–77). Although exopeptidolytic processing of IL-8 up to position 6 by aminopeptidase N (CD13) is quite unlikely out (Proost et al., 2007), the N-terminal pentapeptide of IL-8 could also be clipped off by MMP-8 (Tester et al., 2007). Hence, it remains to be clarified which of the various proteases (i.e., MMP-8, MMP-9, and PR3) are really relevant for this process in vivo.

3. Acute Lung Injury and Acute Respiratory Distress Syndrome. Acute lung injury (ALI) and the acute respiratory distress syndrome (ARDS) are inflammatory disorders of the lung most commonly caused by trauma, sepsis, and pneumonia, the latter two being responsible for approximately 60% of cases (Tsushima et al., 2009). These pathologic conditions are characterized by increased hypoxemia and alveolar-capillary permeability. ALI and ARDS, its most severe form, differ in the degree of hypoxemia. In ARDS, the alveolar-capillary barrier is compromised, resulting in the formation of a protein-rich edema, filling alveoli. Early in the initiation of ALI and ARDS, neutrophils massively accumulate in the vasculature of the lung. Neutrophils and their cytotoxic products, including oxidants and proteases, have central pathological functions in ALI and ARDS. Increased elastolytic activity (Lee et al., 1981), as well as increased levels of oxidative stress, reflected by increased exhalation of H_2O_2 , have been observed in patients with ARDS (Repine, 1992). Increased levels of HNE in plasma and in BAL have also been observed with at-risk patients who later developed ALI (Suter et al., 1992; Donnelly et al., 1995). Pathologic effects of HNE are associated with microvascular injury, causing endothelial damage, increased capillary permeability, and interstitial edema. Oxidants derived from neutrophils and endothelial cells enhance the pathogenic function of HNE because of their ability to oxidatively inactivate endogenous inhibitors. After the formation of the protein-rich edema fluid, HNE can cleave fibrin and $\alpha 1$ -PI to generate potent chemotactic peptides that further contribute to the inflammatory response in the lung (Banda et al., 1988b; Leavell et al., 1996). HNE may also potentiate the inflammatory response by increasing the expression and release of cytokines (Bédard et al., 1993) and by increasing mucin production (Voynow et al., 1999). In experimental animal models, intratracheal administration of exogenous HNE induces lung hemorrhage and ALI, whereas administration of pharmacological HNE inhibitors prevents lung injury, which further supports the role of NSPs in lung injury (Lee and Downey, 2001; Kawabata et al., 2002; Zeiher et al., 2002).

B. Anti-Neutrophil Cytoplasmic Autoantibody-Associated Vasculitides

ANCA-associated vasculitides encompasses a variety of diseases characterized by inflammation of blood vessels and by the presence of autoantibodies directed against neutrophil constituents. These autoantibodies

are known as ANCAs (Kallenberg et al., 2006). In Wegener granulomatosis (WG), antibodies are mostly directed against PR3. WG is a relatively uncommon chronic inflammatory disorder first described in 1931 by Heinz Karl Ernst Klinger as a variant of polyarteritis nodosa (Klinger, 1931). In 1936, the German pathologist Friedrich Wegener described the disease as a distinct pathological entity (Wegener, 1936, 1939). WG is characterized by necrotizing granulomatous inflammation and vasculitis of small vessels and can affect any organ (Fauci and Wolff, 1973; Sarraf and Sneller, 2005). The most common sites of involvement are the upper and lower respiratory tract and the kidneys. WG affects approximately 1 in 20,000 people; it can occur in persons of any age but most often affects those aged 40 to 60 years (Walton, 1958; Cotch et al., 1996). Approximately 90% of patients have cold or sinusitis symptoms that fail to respond to the usual therapeutic measures and that last considerably longer than the usual upper respiratory tract infection. Lung involvement occurs in approximately 85% of the patients. Other symptoms include nasal membrane ulcerations and crusting, saddle-nose deformity, inflammation of the ear with hearing problems, inflammation of the eye with sight problems, and cough (with or without hemoptysis).

The cause of WG has not yet been elucidated, but infection with *S. aureus* could well contribute to its pathogenicity (Kallenberg, 2008). Deficiency in $\alpha 1$ -PI also is a risk factor of WG. Studies of gene polymorphisms showed that the frequency of the $\alpha 1$ -PI deficiency allele PI*Z is increased in WG and is related to its outcome (Esnault et al., 1993; Callea et al., 1997; Needham and Stockley, 2004). WG is characteristically associated with the presence of ANCA, directed against proteins of neutrophilic granulocytes and monocytes stored in cytoplasmic granules (Reumaux et al., 2004; Kallenberg et al., 2006; Kallenberg, 2008). The occurrence of this cytoplasmic staining pattern was first reported in 1982 in patients with necrotizing glomerulonephritis (Davies et al., 1982). Jenne et al. (1990) identified PR3 as the target antigen for ANCA. Though most patients with WG are positive for ANCAs, antibody titer in the serum of patients does not always correlate with the severity of the disease, which raises the question of the pathogenicity of ANCAs (Merkel et al., 2009). In addition to cytoplasmic ANCA (or cANCA, which usually recognizes PR3 in WG), perinuclear ANCA (pANCA) have been demonstrated by enzyme-linked immunosorbent assay and indirect immunofluorescence on ethanol-fixed neutrophils (Hoffman and Specks, 1998). pANCA are predominantly directed against myeloperoxidase but some are also directed against HNE and CG (Savigne et al., 1998) and can additionally be found in a variety of inflammatory diseases, including sometimes Crohn disease, rheumatoid arthritis, and drug-induced vasculitis (Hoffman and Specks, 1998; Radice and Sinico, 2005). The precise subcellular localization resulting in the apparent perinuclear

distribution of pANCA remains uncertain (Yang, 1997; Hoffman and Specks, 1998).

Mouse monoclonal anti-PR3 antibodies and cANCA from WG patients recognize conformational epitopes on PR3 (Bini et al., 1992) that may vary during the course of the disease (Rarok et al., 2003). Four groups of mouse monoclonal anti-PR3 antibodies have been identified. Antibodies in the same group recognize similar epitopes on PR3 (Van Der Geld et al., 1999). Autoantibodies to HNE are responsible for a syndrome of midline destructive vasculitis, which is associated with use of cocaine via nasal insufflations (Wiesner et al., 2004).

Resting neutrophils from purified peripheral blood of healthy persons express PR3 on their membranes in a genetically determined manner, and this proportion of PR3 is increased in a stepwise fashion by neutrophil priming and subsequent activation (Schreiber et al., 2003). Circulating blood neutrophils from patients with active WG express PR3 on their cell membranes in larger quantities than healthy persons as a result of an ongoing inflammatory process (Rarok et al., 2002). Likewise, neutrophils from healthy volunteers can be primed with proinflammatory cytokines (e.g., TNF- α) to increase the fraction of surface-exposed PR3 directly accessible to circulating cANCA (Csernok et al., 1994). Neutrophils become fully activated upon cANCA binding to their membranes. They produce reactive oxygen species and release lysosomal proteases from their azurophilic granules to the pericellular environment. In recent work, Kessenbrock et al. (2009) showed that TNF- α -primed neutrophils stimulated by cANCA produce NET containing PR3 and myeloperoxidase. Deposition of NET in inflamed kidneys and the presence of circulating myeloperoxidase-DNA complexes suggest that NET formation contributes to focal necrotizing glomerulonephritis and enhances the autoimmune response against neutrophil components in individuals with small-vessel vasculitis.

C. Hereditary Neutropenias

Neutropenia is a hematological disorder characterized by an abnormally low number of neutrophils (Horwitz et al., 2007). The normal neutrophil count fluctuates across human populations and within individual patients in response to infection but typically lies in the range of 1.5 to 5×10^9 cells/liter. Neutropenia is categorized as severe when the cell count falls below 0.5×10^9 cells/liter. Hence, patients with neutropenia are more susceptible to bacterial infections and, without prompt medical attention, the condition may become life-threatening. Common causes of neutropenia include cancer chemotherapy, drug reactions, autoimmune diseases, and hereditary disorders (Berliner et al., 2004; Schwartzberg, 2006).

Cyclic neutropenia and severe congenital neutropenia are the two main forms of hereditary neutropenia (Ancliff, 2003; Horwitz et al., 2007). Their prevalence has been estimated at 1 in 200,000 in newborn. Cyclic neu-

tropenia (MIM 162800) is an autosomal disease in which blood-cell production from the bone marrow oscillates with a 21-day periodicity. Circulating neutrophils vary between almost normal numbers and zero. Monocytes also cycle but do so in a phase that is opposite that of neutrophils (Berliner et al., 2004). During neutropenic periods, affected persons are at risk for opportunistic infections (Reimann and DeBerardinis, 1949). The periodic fluctuation between high and low neutrophil counts could be explained by a feedback mechanism through which mature neutrophils inhibit maturation of progenitor cells (Horwitz et al., 2003; Salipante et al., 2009). The first case of human cyclic neutropenia was reported by Leale (1910), but only in 1999 did Horwitz et al. (1999) report that mutations of the elastase gene *ELA2*, since then renamed *ELANE*, were responsible for human cyclic neutropenia.

Severe congenital neutropenia (MIM 202700), also called Kostmann disease, refers to a noncyclic neutropenia present at birth (absolute neutrophil count below 0.5×10^9 /liter). It was first reported as infantile agranulocytosis in a large Swedish family of consanguineous parents (Kostmann, 1956; Carlsson et al., 2006). A characteristic of severe congenital neutropenia is that the bone marrow displays a defect in maturation of developing myeloid cells at the promyelocyte stage. Mutations in *ELANE* are present in approximately 60% of severe congenital neutropenia cases, and approximately 50 different mutations scattered throughout the coding regions have been identified. Many of the mutations do not lead to loss of enzymatic activity (Horwitz et al., 2007). Bioinformatic analysis of different pathogenic missense mutations in *ELANE* suggests diverse deleterious effects on structural and physicochemical properties of HNE (Thusberg and Vihinen, 2006). Additional rare cases of severe congenital neutropenia arise from mutations in the genes encoding zinc finger transcription factor GFI1 (Person et al., 2003), glucose-6-phosphatase (Boztug et al., 2009), and HS1-associated protein X-1 (Klein et al., 2007). Patients with severe congenital neutropenia present symptoms of recurrent bacterial infections mostly in the skin, the respiratory system, and the oral cavity, whereas some patients may also present with severe generalized infections. Neutropenic patients often respond to granulocyte colony-stimulating factor, which stimulates neutrophil production in bone marrow. Bone marrow transplantation is warranted in patients who are unresponsive to granulocyte colony-stimulating factor or who develop leukemia.

The heterotetrameric adaptor protein complex 3 (AP-3) residing on the cytoplasmic surface of intracellular vesicles has been shown to function in the sorting of proteins to the endosomal/lysosomal system (Badolato and Parolini, 2007). Mutation of the gene encoding the AP-3 β subunit, which disrupts the complex, have been found to cause Hermansky Pudlak syndrome type 2 (MIM 203300) (Dell'Angelica et al., 1999; Huizing et al., 2002), a disorder

characterized by oculocutaneous albinism, platelet granular dysfunction, and neutropenic immunodeficiency (Huizing et al., 2008), and also to cause a canine form of cyclic neutropenia associated with pigmentation dilution known as “gray collie syndrome” (Lothrop et al., 1987). Benson et al. (2003) have argued that mutations in either the HNE or AP-3 gene perturbs intracellular trafficking of HNE, implying that mislocalization of HNE may be involved in the pathogenesis of the congenital neutropenias associated with *ELANE* mutations. Alternatively, mutations in *ELANE* may induce the unfolded protein response as a consequence of incorrect folding and targeting of the mutant proteins, with associated programmed cell death (Köllner et al., 2006; Grenda et al., 2007). Expression of mutant HNE, but not wild-type HNE, strongly induced BiP/GRP78 mRNA expression and XBP1 mRNA splicing, two classic markers of the unfolded protein response (Grenda et al., 2007).

D. Papillon-Lefèvre Syndrome

Papillon-Lefèvre syndrome (PLS; MIM 245000) is a hereditary skin disease characterized by a diffuse palmo-plantar keratosis and severe periodontitis, leading to premature loss of both the deciduous and permanent teeth (Dhanrajani, 2009). Approximately 15 to 20% of patients are predisposed to recurrent infections. The combination of oral retinoids and antibiotics complemented with professional tooth cleaning are currently used in the treatment of severe periodontitis occurring with this disorder (Dhanrajani, 2009). PLS is an extremely rare inherited autosomal recessive disease with an estimated prevalence of 1 to 4 cases per million people, affecting children between the ages of 1 and 4 (Gorlin et al., 1964). It was first described by two French physicians, Papillon and Lefèvre (1924), as a form of “Mal de Meleda” and was only later classified as a distinct entity (Dekker and Jansen, 1956). More than 200 cases worldwide have been reported in the literature. Consanguinity of the parents was observed in approximately one third of the cases described. Both sexes are equally affected; no racial predominance seems to exist (Haneke 1979; Hattab et al., 1995). Loss-of-function mutations in the DPPI gene (*CSTC*) on chromosome 11q14-q21 are strongly correlated with PLS and the related Haim-Munk syndrome (Hart et al., 1999, 2000; Toomes et al., 1999).

The exact cause of periodontal disease in PLS has not been elucidated, but it has been attributed to a neutrophil defect resulting in decreased phagocytosis and chemotaxis (Brown et al., 1993; Bullon et al., 1993; Firatli et al., 1996). Association of neutrophil or myeloid abnormalities with severe periodontal destruction and the development of rapid periodontal infections in experimentally induced neutropenia in animals suggest that neutrophils are protective against periodontal destruction. The 116-kDa pore-forming leukotoxin is the prime virulence factor of the periodontopathogen *A. actinomycetemcomitans* and pro-

notes its colonization while inducing granule exocytosis and lysis of primed neutrophils. NSPs degrade this toxin extracellularly (Johansson et al., 2000, 2001). Furthermore, they convert the neutrophil-derived hCAP-18 into LL-37, an antimicrobial peptide with activity against *A. actinomycetemcomitans* (de Haar et al., 2006). In PLS, the loss of DPPI activity within neutrophils results in a severe reduction in the activity and stability of NSPs (Pham et al., 2004; de Haar et al., 2004), leading to the generation of lower levels of LL-37 by neutrophils (de Haar et al., 2006) and reduced efficiency of degradation of leukotoxin produced by *A. actinomycetemcomitans* (de Haar et al., 2006).

Pham et al. (2004) have shown that neutrophils from most patients with PLS display normal microbicidal activity against *E. coli* and *S. aureus* despite their severe deficiency in NSPs, but neutrophils from certain patients were defective in microbial killing. This clinical observation suggests that NSPs are not essential antimicrobial molecules and may explain why only a few patients with PLS demonstrate severe recurrent systemic infections.

VI. New Strategies for Fighting Neutrophil Serine Protease-Related Human Diseases

Administration of therapeutic inhibitors to control unwanted proteolysis at inflammation sites has been tested as a therapy for a variety of inflammatory and infectious lung diseases (Chughtai and O’Riordan, 2004). Depending on the size and chemical nature of the inhibitors, they may be administered orally, intravenously, or by an aerosol route. Whatever the mode of administration, the access of therapeutic inhibitors to active proteases is often hampered by physicochemical constraints in the extravascular space and/or by the partitioning of proteases between soluble and solid phases. These solid structures are, for example, molecular components of the matrix or components of the cellular membranes, NET, proteoglycans, and possibly other macromolecular structures. One way to bypass this possible drawback of inhibitor administration would be to reduce the intracellular level of active NSPs within neutrophils by deregulating their intracellular trafficking, a process that may not affect neutrophil infiltration and accumulation at infectious sites and may therefore maintain their beneficial microbicidal properties. Reduction of neutrophil accumulation at inflammatory sites also seems to be another alternative for reducing extracellular NSP activities during noninfectious diseases, where the presence of neutrophils is a priori not beneficial (Fig. 6).

A. Therapeutic Inhibitors

CF, ALI, and ARDS are characterized by the presence of pathogens in the lung. Migration of neutrophils to sites of infection is beneficial because of their capacity to kill pathogens intracellularly after phagocytosis and ex-

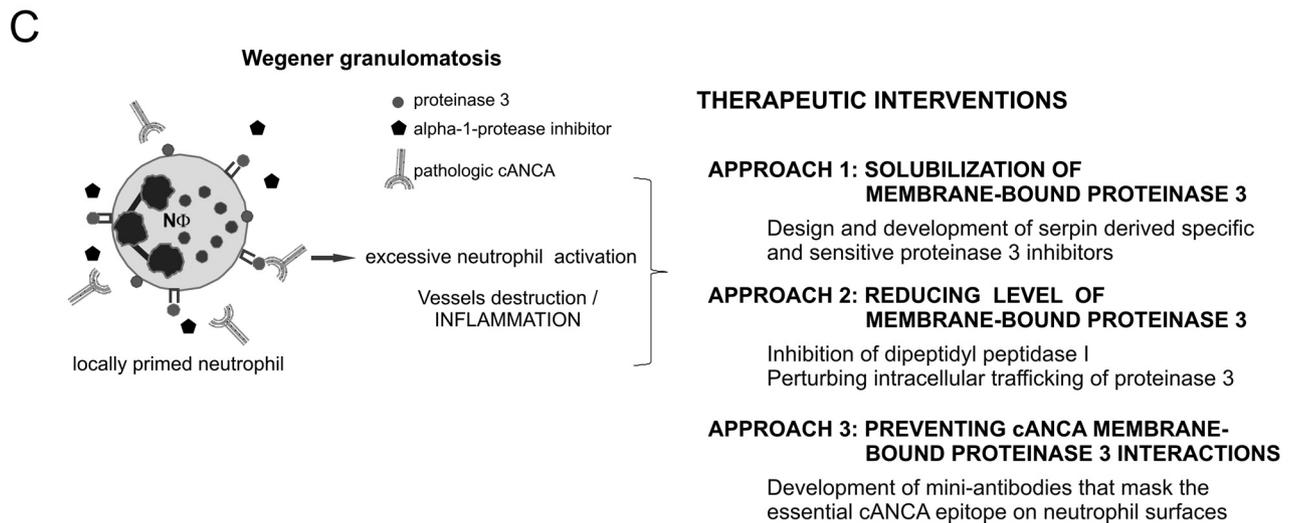
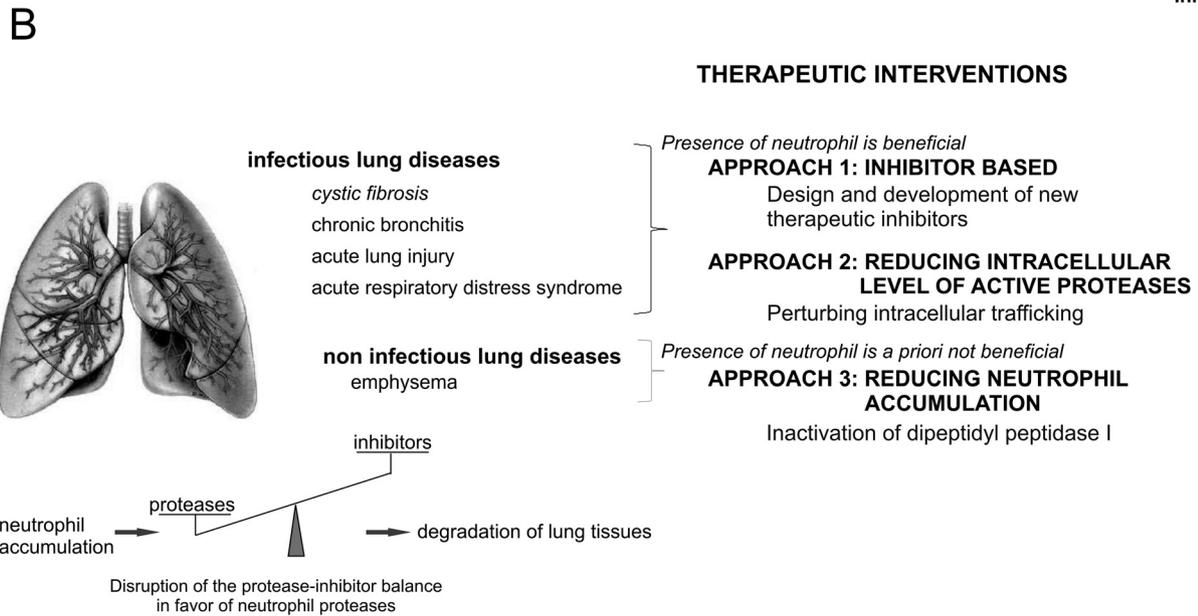
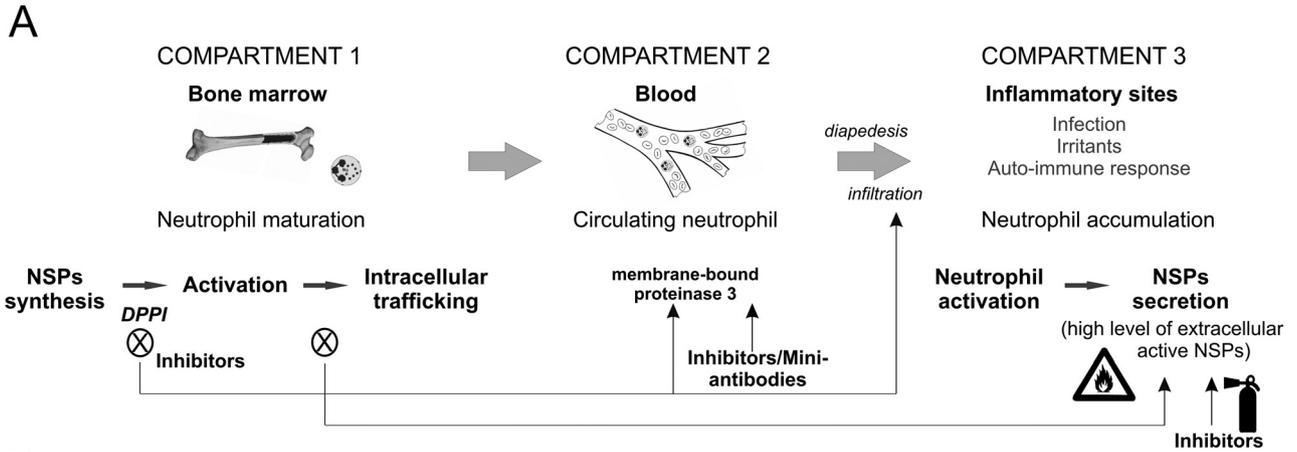


FIG. 6. A, interventional options for the control of neutrophil proteases. The different compartments in which the exposure to NSPs can be reduced and the biological impact of this intervention are shown. B, the different therapeutic approaches to rebalance the altered protease/antiprotease equilibrium in neutrophil-associated inflammatory lung diseases. C, specification for the treatment of Wegener granulomatosis, which is characterized by excessive ANCA-induced activation of locally primed PR3-positive neutrophils and subsequent small vessel destruction.

tracellularly upon release of NET. However, the presence of neutrophils at infection sites may also be deleterious when an excessive, uncontrolled amount of NSP is released into the extracellular medium and leads to lung matrix degradation. Supplementation with exogenous, natural, synthetic, or recombinant NSP inhibitors administered by the vascular route or by aerosols has been tried as a means for restoring the protease/inhibitor balance but without fully convincing results. This is not surprising, however, because 1) exogenous inhibitors do not target all three NSPs released from activated neutrophils, (Owen and Campbell, 1999; Owen, 2008b) and 2) proteolysis in the lung, for example, may occur even in the presence of active endogenous inhibitors as neutrophils adhere to extracellular matrix components and to the vascular endothelium and deposit NSPs in direct proximity to their protein substrates (Owen and Campbell, 1999; Owen, 2008b). Extracellular proteases may also escape inhibition through their association with cell membranes or with negatively charged macromolecular components such as DNA or proteoglycans. Thus, an ideal NSP inhibitor that would control proteolytic activities within given limits should be able to inhibit HNE, PR3, and CG with similar efficiency; would resist rapid oxidation and proteolysis; and would be of small size, thereby affording better access to NSPs when they are bound to extracellular matrices and to molecular or cellular components. It should also resist aerosolization and in vivo degradation. None of the inhibitors developed to fight chronic inflammatory diseases so far address all of these criteria. Nevertheless, replacement therapy by intravenous administration of α 1-PI has long been shown to be efficient for α 1-PI deficiency associated with emphysema (Wewers et al., 1987; Hubbard et al., 1988), and aerosolized administration of α 1-PI or SLPI to patients with cystic fibrosis suppressed or significantly reduced HNE in the respiratory epithelial lining fluid and restored the anti-HNE capacity (McElvaney et al., 1991, 1993). α 1-PI augmentation therapy also abrogates HNE-induced up-regulation of cathepsin B and MMP-2 expression, further demonstrating the central role of this protease as a target in many inflammatory diseases (Geraghty et al., 2007, 2008). A remaining problem, however, is that serpins may have impaired access to the microenvironment created by the contact between neutrophils and proteins of the extracellular matrix because of their large molecular weight and their potential sensitivity to oxidation and proteolysis. On the other hand, therapeutically applied inhibitors should not completely abrogate the putative physiological roles of proteases in the pericellular milieu of the neutrophil. This might happen with inhibitors that instantaneously and irreversibly inactivate the target proteases. Hence, competitive inhibitors that can dissociate from proteases, as after withdrawing inhibitor administration, seem to be more appropriate and better suited to curtail excessive proteolytic activity. Irreversible inhibitors such as ser-

pins, however, may also preserve a basal low level of proteolytic activity provided the delay time for full inhibition is long enough to allow substantial substrate cleavage by the protease before its complete inactivation (Bieth, 1986). The delay time to reach a complete irreversible inhibition depends on the local concentration of the two partners, the association rate constant, and the specificity constant toward the biological substrate. In this way, partial oxidative inactivation of α 1-PI in inflammatory biological fluids contributes to the maintenance of some local HNE activity and its pericellular functions (Luisetti and Travis, 1996). The chemical inhibitor sivelestat and the recombinant low-molecular-weight inhibitor depelstat are resistant to oxidative and proteolytic inactivation but are targeting only HNE (Kawabata et al., 1991; Attucci et al., 2006). Most synthetic and chimeric elastase inhibitors developed so far have not proceeded beyond phase II of development because of side effects in addition to poor efficacy (Tremblay et al., 2003). Polyvalent recombinant protein inhibitors that target all three NSPs have recently been developed (Zani et al., 2009). One is a recombinant chimera resulting from the fusion of the C-terminal domain of SLPI and elafin; the other is a trappin-2 variant in which the P1 residue Ala is replaced by Leu. These recombinant low- M_r proteins are tight-binding inhibitors of all three NSPs, demonstrating nanomolar or subnanomolar K_i values. They inhibit membrane-bound NSPs but do not resist oxidative inactivation because of the presence of a critical methionine residue at the P1' position (Zani et al., 2009). Further investigation is needed to identify critical residues involved in the interaction of each protease with physiological, recombinant, and synthetic inhibitors. Specific and highly sensitive FRET substrates designed and developed to measure the activities of HNE, PR3, and CG at the surface of triggered neutrophils and in whole biological fluids are important tools for quantifying active HNE, PR3, and CG in lung diseases (Korkmaz et al., 2008a). These substrates, allowing measurement of proteolytic activities in both solid and soluble fraction of BAL fluid or sputum from patients with chronic inflammatory diseases, will no doubt aid the investigation of spatiotemporal efficacy of administered therapeutic inhibitors.

cANCA are directed against PR3 and are a diagnostic marker of WG, although cANCAs are not found in approximately 10% of patients with Wegener granulomatosis (Radic and Sinico, 2005). Their simultaneous interaction with mPR3 and Fc receptors is believed to trigger full activation and degranulation of neutrophils around small vessels in patients with active disease (Kallenberg, 2008). Unlike HNE and CG, PR3 is constitutively expressed on the surface of circulating neutrophils but is proteolytically inactive (Korkmaz et al., 2009). This prevents constitutive PR3 from interacting with circulating protease inhibitors but not with cANCAs, which, in turn, may activate neutrophils and favor expression of active NSPs at the cell

surface. Designing a specific PR3 inhibitor that removes active PR3 from the surface of activated neutrophils would probably help reduce ANCA binding to the cell surface and therefore small vessel inflammation. Unfortunately, such an inhibitor is not yet available. The main circulating PR3 inhibitor is α 1-PI, which forms soluble protease-inhibitor complexes but inhibits PR3 at a rate approximately 100 times lower than that of HNE. This may result in a transient increase of active mPR3 on primed neutrophils with cANCA binding and subsequent neutrophil activation. Although it was found that heterozygotes for the P1Z variant of the α 1-PI gene are at greater risk than the general population for developing WG (Elzouki et al., 1994), there is currently no evidence that AAT augmentation therapy is effective in the treatment of WG associated with AAT deficiency (Silverman and Sandhaus, 2009). In keeping with this, we recently found that pathogenic cANCA react with membrane-bound PR3 faster than does α 1-PI (Kuhl et al., 2010), which supports the idea that the inhibitor cannot significantly impair neutrophil triggering by cANCA.

Designing specific inhibitors capable of targeting a particular protease such as PR3 (for the treatment of WG) or polyvalent inhibitors (to improve control of multiple proteases in infectious and inflammatory disorders) requires a deeper investigation of the interaction between protease active sites and inhibitors at the molecular level. Determination of the three-dimensional structures of protease-inhibitor complexes and characterization of protease specificities through kinetic analysis using synthetic substrates has provided information indicating the residues and subsites that are involved in such interactions. A strategy for engineering α 1-PI to become a specific and sensitive inhibitor of PR3 could consist of substituting the exposed reactive center loop of α 1-PI, which could then interact with charged residues present in the active site of PR3. This approach might also help to elucidate the mechanism of degradation by PR3 of the α 1-PI RCL (Duranton and Bieth, 2003). Such a hypothetical recombinant serpin-like inhibitor might be capable of rapidly removing active PR3 from the activated neutrophil membranes and could be helpful in modulating cANCA-neutrophil interactions in WG.

This approach could be extended by development of monoclonal humanized mini antibodies capable of masking the essential cANCA epitope on mPR3, which will impair neutrophil activation. It is noteworthy that monoclonal antibodies represent a promising class of biotherapeutics for the treatment of autoimmune diseases and cancers, and more than 20 mAbs have been approved for therapy or are in clinical trials (Lynch et al., 2009). Rituximab, a chimeric monoclonal antibody directed against CD20, which is present primarily on B cells and is currently used in the treatment of non-Hodgkin's lymphoma and rheumatoid arthritis (Plosker and Figgitt, 2003; Fleischmann, 2009), significantly decreases the level of anti PR3 autoantibodies, resulting in

patient clinical remission (Ferraro et al., 2008) that is possibly related to a lower neutrophil activation.

B. Reducing Intracellular Levels of Active Elastase, Proteinase 3, and Cathepsin G

Impairment of access of therapeutic inhibitors to extracellularly active NSPs represents a possible limitation of an inhibitor-based approach to the treatment of infectious and inflammatory pulmonary diseases. This may occur both because of the composition of the extracellular medium (mucus, NET, proteoglycans, and other macromolecules) and because of the spatiotemporal localization of NSPs. Reducing the intracellular levels of active NSPs in mature neutrophils, without perturbing their functions and accumulation at infectious sites, in theory, represents an alternative approach for limiting uncontrolled proteolysis (Fig. 6). Potentially, this could be achieved through disruption of the intracellular trafficking of mature NSPs. A decrease in the immune reactive level of NSPs is observed when intracellular proteins involved in protein sorting and vesicle transport are mutated in human diseases. Mutations of the AP-3 cargo protein and of the CHS protein in Hermansky Pudlak syndrome-2 and Chediak-Higashi syndrome, respectively, result in decreased intracellular levels of HNE and CG (Ganz et al., 1988; Fontana et al., 2006). AP-3 cargo protein and the CHS protein are believed to be involved in vesicle formation and transport. A low HNE level is also observed in neutrophils from neutropenia patients with HS1-associated protein X-1 mutations (B. Korkmaz and M. S. Horwitz, unpublished results). The proteoglycan serglycin has recently been shown to play a role in the sorting of NE (Niemann et al., 2007). In serglycin knockout mice, NE is absent from mature neutrophils but serglycin inactivation has no effect on correct granular targeting and on intracellular quantities of CG and PR3. Furthermore, the lack of serglycin has no effect on neutrophil count and ultrastructure (Niemann et al., 2007), demonstrating that inactivation of a protein involved in the sorting of NE does not necessarily induce neutropenia, whereas dysfunctional AP3 and CHS proteins impair granule formation and protein targeting in general. Thus, there is cumulative evidence that the intracellular level of HNE and possibly of other related NSPs depends on the functionality of molecules involved in its intracellular trafficking.

Identifying and inactivating other molecular targets that deregulate protease trafficking without inducing neutropenia or altering neutrophil function or chemotaxis could possibly be exploited for a therapeutic strategy aiming at controlling the production and the activity of NSPs in chronic inflammatory lung diseases. It has been shown, however, that NSPs liberated at the inflammatory sites regulate local production of cytokines, leading to neutrophil infiltration and accumulation. In fact, neutrophil infiltration at sites of inflammation is severely diminished in PR3(-/-)/NE(-/-) mice un-

less only NE is deficient (Kessenbrock et al., 2008). In that case, neutrophil infiltration and accumulation is only marginally affected. Because both PR3 and NE in mice share similar active sites (Fig. 5) and are able to activate proinflammatory cytokines IL-8 and IL-1 β , it can be concluded that only one is necessary to promote neutrophil recruitment at inflammatory sites. In humans, however, IL-8 and IL-1 β are specifically activated by human PR3. This means that altered intracellular trafficking of HNE is not expected to modify neutrophil migration toward inflammatory sites. Using an animal (primate) model in which the NSP specificities are closer to those in humans should permit the testing of this hypothesis.

C. Reducing Neutrophil Accumulation at Inflammatory Sites

In noninfectious lung diseases and other inflammatory human diseases characterized by an excessive neutrophil accumulation, such as rheumatoid arthritis and inflammatory bowel diseases, containment of NSP activities could occur before proteases are released from neutrophils at the inflammatory site (Fig. 6). Strategies for impairing inflammatory cell recruitment to the lung have already been proposed and explored *in vitro* and *in vivo*. For example, inhibitors of phosphodiesterase E4 (PDE4) prevent hydrolysis of cAMP in inflammatory cells, thus reducing their chemoattractant and protease-secreting function (Fan Chung, 2006). By suppressing the release of inflammatory signals, PDE4 inhibitors display a high therapeutic potential in COPD and asthma (Schmidt et al., 1999; Giembycz, 2002). Intraperitoneal administration of the PDE4 inhibitor Rolipram in mice receiving an intranasal challenge of LPS significantly reduces neutrophil accumulation in the lungs (H. Korideck and J. D. Peterson, unpublished data). This observation holds true for mice undergoing long-term exposure to cigarette smoke and treated orally with the long-acting PDE4 inhibitor roflumilast (Martorana et al., 2005). Anti-oxidant supplementation, to block the transcription factor NF- κ B (Szulakowski et al., 2006) and thus the production of several pro-inflammatory molecules causing lung inflammation, also reduces the accumulation of inflammatory cells, and the same result is obtained using inhibitors of chemokine receptors (Donnelly and Barnes, 2006).

DPPI is the major protease involved in the activation of NSPs; it also influences the total intracellular levels of these proteases, as observed in neutrophils from patients with PLS (Pham et al., 2004). In addition, mice deficient in DPPI demonstrate impaired neutrophil accumulation in their joints in response to noninfectious inflammatory stimuli but are protected against cartilage destruction in acute arthritis experimentally induced by immune complexes (Adkison et al., 2002). The decrease in neutrophil accumulation in DPPI(-/-) mice is correlated with cytokine/chemokine dysregulation at inflam-

matory sites resulting from the absence of proteolytically active NSPs (Adkison et al., 2002; Akk et al., 2008). In patients with PLS, DPPI deficiency leads to the accumulation of neutrophils in the blood as they are hampered to enter the extravascular tissue. Taken together, these observations support the idea that DPPI inhibitors could be useful for the treatment of a number of important inflammatory diseases, including lung diseases. Using such inhibitors in infectious diseases, on the other hand, seems to be risky because efficient elimination of pathogens requires both efficient neutrophil recruitment to the site of microbial invasion and rapid destruction of microbes in phagolysosomes. As a significant number of PLS patients display a normal anti-microbial response to common pathogens, NSPs are presumably not essential to overcome invading pathogens (Pham, 2006). Hence, redundancy in antimicrobial defense systems provides a favorable window for the application of NSP inhibitors. In a therapeutic inhibitor-based approach, DPPI may be specifically targeted and inactivated in the bone marrow. DPPI inhibition can be achieved with general inhibitors of cysteine proteases such as diazomethyl ketones, dipeptide nitriles, vinylsulfones, and (2S,3S)-3-[[[(1S)-1-[[[4-[(aminoiminomethyl)amino]butyl]amino]carbonyl]-3-methylbutyl]amino]carbonyl]-2-oxiranecarboxylic acid (E-64) (Barrett et al., 1982; McGuire et al., 1992; Méthot et al., 2007). Among the existing inhibitors, Gly-Phe-diazomethylketone is one of the most effective compounds (Kam et al., 2004; Méthot et al., 2007). Dipeptide nitriles and vinyl sulfone inhibitors are nontoxic to cells and effective toward intracellular DPPI and are therefore potentially suitable for functional studies. Long-term administration of a dipeptide nitrile DPPI inhibitor transported by a poly(ethylene glycol)-based vehicle results in the nearly complete inhibition of DPPI and causes marked reduction of neutrophil accumulation at inflammatory site (Méthot et al., 2008). Specific, nontoxic inhibitors of DPPI may be delivered to the bone marrow by liposomal formulations originally developed for the treatment of leukemias (Gregoriadis et al., 1974; Kohlschütter et al., 2008). As a consequence of therapeutic DPPI inhibition, pro-NSPs would not be converted into active enzymes and that in turn would modulate the levels of inflammatory mediators, such that neutrophils will not infiltrate and accumulate at inflammatory sites. *In vivo* inhibition of NSP activation by targeting DPPI requires high fractional inhibition of this protease in the bone marrow (Méthot et al., 2008). Because mature neutrophils are released from the bone marrow into the peripheral circulation after approximately 11 to 14 days of development (Walker and Willemze, 1980), a continuous administration of DPPI inhibitor over this period would probably be required. Possible side effects of such a prolonged administration cannot be predicted yet, because severe periodontitis and hyperkeratosis, as found in DPPI-deficient patients with PLS, are not observed in mice successfully

treated with DPPI inhibitor to prevent NSP activation (Méthot et al., 2008).

Loss-of-function mutations in DPPI have provided important insight into its role in inflammation, but little information is available on intracellular NSP activation during neutrophil development. Hematopoietic cell lines that express DPPI and are able to activate and target NSPs in a fashion similar to that of human neutrophils represent good models for analyzing the processing of proenzymes by DPPI. The HL-60 (human promyelocytic leukemia cells) cell line contains DPPI and expresses HNE, PR3, and CG (Meagher and Cotter, 1988; Bories et al., 1989; Yoshimura and Crystal, 1992). But other mammalian hematopoietic cell lines [rat basophilic leukemia cells (RBL-1), murine 32D cells and the mast cell line-1] produce DPPI and can be transfected to produce active NSPs that will be stored in granules in a similar fashion as in human neutrophils (Gullberg et al., 1994, 1995; Specks et al., 1996; Garwicz et al., 1997; Li and Horwitz, 2001). Generally, processing and targeting is more rapid and efficient in RBL-1 cells than in other cell lines. Thus, RBL-1 cells have been successfully used to investigate NSP activation by DPPI and to study the influence of HNE mutations on the intracellular trafficking of the protease. Identification of the location of rat DPPI and its colocalization with active HNE by fluorescence microscopy may lead to a better understanding of where pro-NSPs are activated, a question remaining unanswered until now. To this end, chemical fluorescent tracers that irreversibly inactivate human NSPs could be used.

Recently, we showed that pharmacological inactivation of DPPI in RBL cells transfected with HNE impairs HNE targeting to the nuclear envelope and the same result was seen using neutrophils purified from patients with DPPI mutations (B. Korkmaz and M. S. Horwitz, unpublished results). PR3 transfected into RBL-1 cells is present in lysosomes but also on cellular surfaces. One might expect that inactivation of intracellular DPPI by cell permeable inhibitors could well reduce the interaction of PR3 with cellular membranes, because purified pro-PR3 displays less affinity to cellular surfaces than mature PR3 (Korkmaz et al., 2008b). This may be of major importance in WG, because it would allow for a reduction in membrane binding of pathogenic autoantibodies, which results in neutrophil priming and activation.

VII. Concluding Remarks

NSPs were first recognized as protein-degrading enzymes but have now proven to be multifunctional components participating in a variety of pathophysiological processes. Thus, they appear as potential therapeutic targets for drugs that inhibit their active site or impair activation from their precursor. Overall, the available preclinical and clinical data suggest that inhibition of NSPs using therapeutic inhibitors would suppress or

attenuate deleterious effects of inflammatory diseases, including lung diseases. Depending on the size and chemical nature of inhibitors, those may be administered orally, intravenously, or by aerosolization. But the results obtained until now have not been fully convincing because of the poor knowledge of the biological function of each protease, their spatiotemporal regulation during the course of the disease, the physicochemical constraints associated with inhibitor administration, or the use of animal models in which NSP regulation and specificity differ from those in human. Two different and complementary approaches may help bypass these putative problems. One is to target active proteases by inhibitors at the inflammatory site in animal models in which lung anatomy and physiology are close to those in human to allow in vitro and in vivo assays of human-directed drugs/inhibitors. The other is to prevent neutrophil accumulation at inflammatory sites by impairing production of proteolytically active NSPs using an inhibitor of their maturation protease, DPPI. Preventing neutrophil accumulation at the inflammatory sites by therapeutic inhibition of DPPI represents an original and novel approach, the exploration of which has just started (Méthot et al., 2008). Thus pharmacological inactivation of DPPI in human neutrophils could well reduce membrane binding of PR3 and, as a consequence, neutrophil priming by pathogenic auto-antibodies in WG. In addition, it has been recognized that the intracellular level of NSPs depends on their correct intracellular trafficking. In the future, pharmacological targeting of molecules specifically involved in the correct intracellular trafficking of each NSP could possibly regulate their production and activity, a feature that could be exploited as a therapeutic strategy for inflammatory diseases.

Although rodent models of human diseases have largely contributed to progress in biomedical sciences for studying disease pathogenesis and identifying and testing novel therapeutic strategies, there are numerous examples showing that they cannot always provide fully reliable answers transferable to humans. For example, transgenic mice with a disrupted *CFTR* gene do not develop the typical manifestations of CF (Snouwaert et al., 1992) and mice exposed to cigarette smoke do not reproduce the exacerbation phases observed with COPD. Furthermore, we recently showed that NSPs in humans and mice demonstrate a slightly different specificity sufficient to prevent some putatively therapeutic human NSPs inhibitors from interacting with mouse proteases (Kalupov et al., 2009). Mouse cANCA serum generated by immunization of PR3(-/-)/NE(-/-) mice murine PR3 does not reproduce pathological features of WG when transferred to systemically lipopolysaccharide-primed wild-type mice (Pfister et al., 2004). The hydrophobic patch mediating membrane expression of human PR3, however, is substituted by highly hydrophilic residues on mouse PR3 (Korkmaz et al., 2008b). Sequence differences between human and mouse may

result in absent or highly reduced mouse PR3 expression at the membrane of neutrophils, which may explain the minor pathogenic effect of antibodies to mouse PR3 in experimental *in vivo* models. Unlike mouse PR3-directed ANCA, antibodies directed against mouse myeloperoxidase produce small-vessel vasculitis upon injection into wild-type mice (Xiao et al., 2002; Kain et al., 2010). Gene-targeted mice carrying the elastase mutation observed in patients with neutropenia (Grenda et al., 2007) or deficient in the DPPI gene do not present the same phenotypical characteristics as those observed in humans (Adkison et al., 2002). Using nonhuman primate models in which NSPs are closer to human homologs at both the structural and functional levels would probably help to circumvent these difficulties and permit exploration of new therapeutic strategies for NSP-related diseases. Nonhuman primates are already explored as experimental models in a variety of human diseases (diabetes, cardiovascular dysfunction, osteoporosis, reproductive senescence, neurobiological aging, and related cognitive decline (Lane, 2000; Brok et al., 2001). The first transgenic primate (*Macaca mulatta*) carrying a dysfunctional gene has been generated (Yang et al., 2008). This transgenic primate presents the symptoms of human Huntington disease, whereas the corresponding mutation of the same gene in mouse does not induce the brain changes and behavioral features observed in humans (Yang et al., 2008). This pioneering work should pave the way for further investigation in this direction particularly for analyzing the function of NSPs in primates with dysfunctional NSP genes.

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